



#7

## SEQUENCE LISTING

<110> CuraGen Corporation  
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<120> Novel Proteins and Nucleic Acids Encoding Same

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<140> 09/825,751

<141> 2001-04-03

<150> 60/194,314

<151> 2000-04-03

<150> 60/225,693

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<170> PatentIn Ver. 2.1

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Gly Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln	
865 870 875	
tgc tcc tgc cat gcc ggc ttc cag agc aca cct gac cgc cag ggc tgc	2687
Cys Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys	
880 885 890 895	
gtg gac atc aac gaa tgc cgg gtc cag aat ggt ggg tgt gac gtg cac	2735
Val Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His	
900 905 910	
cgt att aac act gag ggc agc tac cgg tgc agc tgt ggg cag ggc tac	2783
Arg Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr	
915 920 925	
tcg ctg atg ccc gac gga agg gca tgt gca gac gtg gac gag tgt gaa	2831
Ser Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu	
930 935 940	
gag aac ccc cgc gtt tgt gac caa ggc cac tgc acc aac atg cca ggg	2879
Glu Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly	
945 950 955	
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Gly His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met	
960 965 970 975	
agg aca tgt gtt gat gtg gat gag tgt gac ctg aac cct cac atc tgc	2975
Arg Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys	
980 985 990	
ctc cat ggg gac tgc gag aac acg aag ggt tcc ttt gtc tgc cac tgt	3023
Leu His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys	
995 1000 1005	
cag ctg ggc tac atg gtc agg aag ggg gcc aca ggc tgc tct gat gtg	3071
Gln Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val	
1010 1015 1020	

gat gaa tgc gag gtt gga gga cac aac tgt gac agt cac gcc tcc tgt 3119  
Asp Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys  
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ctc aac atc ccg ggg agt ttc agc tgt agg tgc ctg cca ggc tgg gtg 3167  
Leu Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val  
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Gly Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu  
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cac cgg tgc agc cca aga ggt gac tgt ctc aat gtc cct ggc tcc tac 3263  
His Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr  
1075 1080 1085  
  
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Arg Cys Thr Cys Arg Gln Gly Phe Ala Gly Asp Gly Phe Phe Cys Glu  
1090 1095 1100  
  
gac agg gat gaa tgt gcc gag aac gtg gac ctc tgt gac aac ggg 3356  
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Arg Ala Gly Ala Cys Phe Ser Val Leu Phe Gly Gly Arg Cys Ala Gly  
35 40 45  
  
Asp Leu Ala Gly His Tyr Thr Arg Arg Gln Cys Cys Cys Asp Arg Gly  
50 55 60  
  
Arg Cys Trp Ala Ala Gly Pro Val Pro Glu Leu Cys Pro Pro Arg Gly  
65 70 75 80

Ser Asn Glu Phe Gln Gln Leu Cys Ala Gln Arg Leu Pro Leu Leu Pro  
 85 90 95

Gly His Pro Gly Leu Phe Pro Gly Leu Leu Gly Phe Gly Ser Asn Gly  
 100 105 110

Met Gly Pro Pro Leu Gly Pro Ala Arg Leu Asn Pro His Gly Ser Asp  
 115 120 125

Ala Arg Gly Ile Pro Ser Leu Gly Pro Gly Asn Ser Asn Ile Gly Thr  
 130 135 140

Ala Thr Leu Asn Gln Thr Ile Asp Ile Cys Arg His Phe Thr Asn Leu  
 145 150 155 160

Cys Leu Asn Gly Arg Cys Leu Pro Thr Pro Ser Ser Tyr Arg Cys Glu  
 165 170 175

Cys Asn Val Gly Tyr Thr Gln Asp Val Arg Gly Glu Cys Ile Asp Val  
 180 185 190

Asp Glu Cys Thr Ser Ser Pro Cys His His Gly Asp Cys Val Asn Ile  
 195 200 205

Pro Gly Thr Tyr His Cys Arg Cys Tyr Pro Gly Phe Gln Ala Thr Pro  
 210 215 220

Thr Arg Gln Ala Cys Val Asp Val Asp Glu Cys Ile Val Ser Gly Gly  
 225 230 235 240

Leu Cys His Leu Gly Arg Cys Val Asn Thr Glu Gly Ser Phe Gln Cys  
 245 250 255

Val Cys Asn Ala Gly Phe Glu Leu Ser Pro Asp Gly Lys Asn Cys Val  
 260 265 270

Asp His Asn Glu Cys Ala Thr Ser Thr Met Cys Val Asn Gly Val Cys  
 275 280 285

Leu Asn Glu Asp Gly Ser Phe Ser Cys Leu Cys Lys Pro Gly Phe Leu  
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Leu Ala Pro Gly Gly His Tyr Cys Met Asp Ile Asp Glu Cys Gln Thr  
 305 310 315 320

Pro Gly Ile Cys Val Asn Gly His Cys Thr Asn Thr Glu Gly Ser Phe  
 325 330 335

Arg Cys Gln Cys Leu Gly Gly Leu Ala Val Gly Thr Asp Gly Arg Val  
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 Cys Val Asp Thr His Val Arg Ser Thr Cys Tyr Gly Ala Ile Glu Lys  
 355 360 365  
 Gly Ser Cys Ala Arg Pro Phe Pro Gly Thr Val Thr Lys Ser Glu Cys  
 370 375 380  
 Cys Cys Ala Asn Pro Asp His Gly Phe Gly Glu Pro Cys Gln Leu Cys  
 385 390 395 400  
 Pro Ala Lys Asn Ser Ala Glu Phe Gln Ala Leu Cys Ser Ser Gly Leu  
 405 410 415  
 Gly Ile Thr Thr Asp Gly Arg Asp Ile Asn Glu Cys Ala Leu Asp Pro  
 420 425 430  
 Glu Val Cys Ala Asn Gly Val Cys Glu Asn Leu Arg Gly Ser Tyr Arg  
 435 440 445  
 Cys Val Cys Asn Leu Gly Tyr Glu Ala Gly Ala Ser Gly Lys Asp Cys  
 450 455 460  
 Thr Asp Val Asp Glu Cys Ala Leu Asn Ser Leu Leu Cys Asp Asn Gly  
 465 470 475 480  
 Trp Cys Gln Asn Ser Pro Gly Ser Tyr Ser Cys Ser Cys Pro Pro Gly  
 485 490 495  
 Phe His Phe Trp Gln Asp Thr Glu Ile Cys Lys Asp Val Asp Glu Cys  
 500 505 510  
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 515 520 525  
 Tyr Thr Cys Lys Cys Gly Pro Gly Ser Arg Leu Asp Pro Ser Gly Thr  
 530 535 540  
 Phe Cys Leu Asp Ser Thr Lys Gly Thr Cys Trp Leu Lys Ile Gln Glu  
 545 550 555 560  
 Ser Arg Cys Glu Val Asn Leu Gln Gly Ala Ser Leu Arg Ser Glu Cys  
 565 570 575  
 Cys Ala Thr Leu Gly Ala Ala Trp Gly Ser Pro Cys Glu Arg Cys Glu  
 580 585 590



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Cys	Asp	Asp	Val	Asn	Glu	Cys	Glu	Ser	Phe	Pro	Gly	Val	Cys	Pro	Asn		
	610					615					620						
Gly	Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Phe	Arg	Cys	Glu	Cys	Pro	Glu		
625					630					635					640		
Gly	Leu	Met	Leu	Asp	Ala	Ser	Gly	Arg	Leu	Cys	Val	Asp	Val	Arg	Leu		
				645					650					655			
Glu	Pro	Cys	Phe	Leu	Arg	Trp	Asp	Glu	Asp	Glu	Cys	Gly	Val	Thr	Leu		
			660					665					670				
Pro	Gly	Lys	Tyr	Arg	Met	Asp	Val	Cys	Cys	Cys	Ser	Ile	Gly	Ala	Val		
	675						680					685					
Trp	Gly	Val	Glu	Cys	Glu	Ala	Cys	Pro	Asp	Pro	Glu	Ser	Leu	Glu	Phe		
	690					695					700						
Ala	Ser	Leu	Cys	Pro	Arg	Gly	Leu	Gly	Phe	Ala	Ser	Arg	Asp	Phe	Leu		
705					710					715					720		
Ser	Gly	Arg	Pro	Phe	Tyr	Lys	Asp	Val	Asn	Glu	Cys	Lys	Val	Phe	Pro		
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Gly	Leu	Cys	Thr	His	Gly	Thr	Cys	Arg	Asn	Thr	Val	Gly	Ser	Phe	His		
			740					745					750				
Cys	Ala	Cys	Ala	Gly	Gly	Phe	Ala	Leu	Asp	Ala	Gln	Glu	Arg	Asn	Cys		
	755						760					765					
Thr	Asp	Ile	Asp	Glu	Cys	Arg	Ile	Ser	Pro	Asp	Leu	Cys	Gly	Gln	Gly		
	770					775					780						
Thr	Cys	Val	Asn	Thr	Pro	Gly	Ser	Phe	Glu	Cys	Glu	Cys	Phe	Pro	Gly		
785					790					795					800		
Tyr	Glu	Ser	Gly	Phe	Met	Leu	Met	Lys	Asn	Cys	Met	Asp	Val	Asp	Glu		
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Cys	Ala	Arg	Asp	Pro	Leu	Leu	Cys	Arg	Gly	Gly	Thr	Cys	Thr	Asn	Thr		
			820					825					830				
Asp	Gly	Ser	Tyr	Lys	Cys	Gln	Cys	Pro	Pro	Gly	His	Glu	Leu	Thr	Ala		
	835						840					845					

Lys Gly Thr Ala Cys Glu Asp Ile Asp Glu Cys Ser Leu Ser Asp Gly  
 850 855 860

Leu Cys Pro His Gly Gln Cys Val Asn Val Ile Gly Ala Phe Gln Cys  
 865 870 875 880

Ser Cys His Ala Gly Phe Gln Ser Thr Pro Asp Arg Gln Gly Cys Val  
 885 890 895

Asp Ile Asn Glu Cys Arg Val Gln Asn Gly Gly Cys Asp Val His Arg  
 900 905 910

Ile Asn Thr Glu Gly Ser Tyr Arg Cys Ser Cys Gly Gln Gly Tyr Ser  
 915 920 925

Leu Met Pro Asp Gly Arg Ala Cys Ala Asp Val Asp Glu Cys Glu Glu  
 930 935 940

Asn Pro Arg Val Cys Asp Gln Gly His Cys Thr Asn Met Pro Gly Gly  
 945 950 955 960

His Arg Cys Leu Cys Tyr Asp Gly Phe Met Ala Thr Pro Asp Met Arg  
 965 970 975

Thr Cys Val Asp Val Asp Glu Cys Asp Leu Asn Pro His Ile Cys Leu  
 980 985 990

His Gly Asp Cys Glu Asn Thr Lys Gly Ser Phe Val Cys His Cys Gln  
 995 1000 1005

Leu Gly Tyr Met Val Arg Lys Gly Ala Thr Gly Cys Ser Asp Val Asp  
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Glu Cys Glu Val Gly Gly His Asn Cys Asp Ser His Ala Ser Cys Leu  
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Asn Ile Pro Gly Ser Phe Ser Cys Arg Cys Leu Pro Gly Trp Val Gly  
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Asp Gly Phe Glu Cys His Asp Leu Asp Glu Cys Val Ser Gln Glu His  
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Arg Cys Ser Pro Arg Gly Asp Cys Leu Asn Val Pro Gly Ser Tyr Arg  
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    1           5           10          15

aac cac agg gac gtg tac ggt ggc atc atc tcc ccc tcc atg ctc tgc 97
Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu Cys
    20           25           30

gcg ggc tac ctg acg ggt ggc gtg gac agc tgc cag ggg gac agc ggg 145
Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
    35           40           45

ggg ccc ctg gtg tgt caa gag agg agg ctg tgg aag tta gtg gga gcg 193
Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala
    50           55           60

acc agc ttt ggc atc ggc tgc gca gag gtg aac aag cct ggg gtg tac 241
Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr
    65           70           75           80

acc gtg tca cct cct tcc tgg act gga tcc acg agc aga tgg aga gag 289
Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu
    85           90           95

acc taaaaacctg aagaggaagg ggataagtag ccacctgagt tcctgaggtg 342
Thr

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ccttgagact ctgagttccg gcaccagtag caggccc 439
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 Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly  
 35 40 45  
 Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala  
 50 55 60  
 Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr  
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 Thr Val Ser Pro Pro Ser Trp Thr Gly Ser Thr Ser Arg Trp Arg Glu  
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 aaa tca gtt gcc gga cta acc atg acc tat gat gga aat aat cca gtg 95  
 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val  
 20 25 30  
 aca tct cat aga gat gtg cca ctt tct tat tgc aac tca gac tgc aat 143  
 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn

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tgt gat gaa agt cag tgg gaa cca gtc tgt ggg aac aat gga ata act			191
Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr			
50	55	60	
tac ctg tca cct tgt cta gca gga tgc aaa tcc tca agt ggt att aaa			239
Tyr Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys			
65	70	75	
aag cat aca gtg ttt tat aac tgt agt tgt gtg gaa gta act ggt ctc			287
Lys His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu			
80	85	90	95
cag aac aga aat tac tca gcg cac ttg ggt gaa tgc cca aga gat aat			335
Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn			
100	105	110	
act tgt aca agg aaa ttt ttc atc tat gtt gca att caa gtc ata aac			383
Thr Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn			
115	120	125	
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Ser Leu Phe Ser Ala Thr Gly Gly Thr			
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Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys			
35	40	45	
Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr			
50	55	60	
Leu Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Ile Lys Lys			
65	70	75	80

His Thr Val Phe Tyr Asn Cys Ser Cys Val Glu Val Thr Gly Leu Gln  
                     85                    90                    95  
 Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asn Thr  
                     100                    105                    110  
 Cys Thr Arg Lys Phe Phe Ile Tyr Val Ala Ile Gln Val Ile Asn Ser  
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 Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro  
                     20                    25                    30  
  
 caa ctc ttc cag gat gac gac gtc ggg gcc gat gag gaa gag gca gag 143  
 Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu  
                     35                    40                    45  
  
 ttg cgg ggc gaa cac acg ctc aca gag aag ttt gtc tgc ctg gat gac 191  
 Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp  
                     50                    55                    60  
  
 tcc ttt ggc cat gac tgc agc ttg acc tgt gat gac tgc agg aac gga 239  
 Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly  
                     65                    70                    75  
  
 ggg acc tgc ctc ctg ggc ctg gat ggc tgt gat tgc ccc gag ggg tgg 287  
 Gly Thr Cys Leu Leu Gly Leu Asp Gly Cys Asp Cys Pro Glu Gly Trp  
       80                    85                    90                    95

act ggg gtt att tgc aat gag att tgt cct ccg ga 322  
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 Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu Leu  
 35 40 45  
 Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp Ser  
 50 55 60  
 Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly Gly  
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cag ggc gcc ctg gac gcc tgc gca cag cga caa ttg caa ttg gag cag	97
Gln Gly Ala Leu Asp Ala Cys Ala Gln Arg Gln Leu Gln Leu Glu Gln	
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agc ctg cgc gtt tgc cgt cgg ctg ctg cat gcc tgg gaa cca act ggg	145
Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly	
35 40 45	
acc cgg gct ttg aag cca cct cca ggg cca gaa act aat gga gag gac	193
Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp	
50 55 60	
ccc ctt cca gca tgc aca ccc agt cca caa gac ctc aaa gag ttg gag	241
Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu	
65 70 75 80	
ttt ctg acc cag gca ctg gag aag gct gta cga gtt cga aga ggc atc	289
Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile	
85 90 95	
act aag gcc gaa gag aga gac aag gcc ccc agc ctg aaa tct agg tcc	337
Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser	
100 105 110	
att gtc acc tct tct ggc acg aca gcc tcc gcc cca ccg cat tcc cca	385
Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro	
115 120 125	
ggc caa gct ggt ggc cat gct tca gac acg aga ccc acc aag ggc ctc	433
Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu	
130 135 140	
cgc cag acc acg gtg cct gcc aag ggc cac cct gag cgc cgg ctg ctg	481
Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu	
145 150 155 160	
tca gtg ggg gat ggg acc cgt gtt ggg atg gga gcc cga acc ccc agg	529
Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg	
165 170 175	
cct ggg gcg ggc ctc agg gac cag caa atg gcc cca tcc gct gct cct	577
Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro	
180 185 190	
cag gcc cca gaa gcc ttc aca ctc aag gag aag ggg cac ctg ctg cgg	625
Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg	
195 200 205	



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Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp	
210 215 220	
gcc cag ctc agt tcc aca cag acc agt gat tcc acg gat gcc gcc gct	721
Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala	
225 230 235 240	
gcc aaa acc cag ttc ctc cag aac atg cag aca gct tca ggc ggg ccc	769
Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro	
245 250 255	
cag ccc agg ctc agt gct gtg gag gtg gag gcg gag gcg ggg cgc ctg	817
Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu	
260 265 270	
cgg aag gcc tgc tcg ctg ctg aga ctg cgc atg agg gag gag ctc tca	865
Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser	
275 280 285	
gca gcc ccc atg gac tgg atg cag gag tac cgc tgc ctg ctc acg ctg	913
Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu	
290 295 300	
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Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu	
305 310 315 320	
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Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly	
325 330 335	
agg ccc ccc gga gcc tcg ccg tcc tgt ggg ggt aga gcg gag cct gca	1057
Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala	
340 345 350	
tgg agc ccc cag ctg ctt gtc tac tcc agc acc cag gag ctg cag acc	1105
Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr	
355 360 365	
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Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His	
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Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala	
385 390 395 400	

cag ccg cag ggg ccg ccc tgg ctg gcc ctg tgc cgg gct gtg cac agc 1249  
 Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser  
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ctg ctc tgc gag gga gga gca cgt gtc ctt acc atc ctg cgg gat gaa 1297  
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                   20                  25                  30

Ser Leu Arg Val Cys Arg Arg Leu Leu His Ala Trp Glu Pro Thr Gly  
                   35                  40                  45

Thr Arg Ala Leu Lys Pro Pro Pro Gly Pro Glu Thr Asn Gly Glu Asp  
                   50                  55                  60

Pro Leu Pro Ala Cys Thr Pro Ser Pro Gln Asp Leu Lys Glu Leu Glu  
   65                  70                  75                  80

Phe Leu Thr Gln Ala Leu Glu Lys Ala Val Arg Val Arg Arg Gly Ile  
                   85                  90                  95

Thr Lys Ala Glu Glu Arg Asp Lys Ala Pro Ser Leu Lys Ser Arg Ser  
                   100                  105                  110

Ile Val Thr Ser Ser Gly Thr Thr Ala Ser Ala Pro Pro His Ser Pro  
                   115                  120                  125

Gly Gln Ala Gly Gly His Ala Ser Asp Thr Arg Pro Thr Lys Gly Leu  
                   130                  135                  140

Arg Gln Thr Thr Val Pro Ala Lys Gly His Pro Glu Arg Arg Leu Leu  
   145                  150                  155                  160

Ser Val Gly Asp Gly Thr Arg Val Gly Met Gly Ala Arg Thr Pro Arg  
 165 . 170 . 175  
 Pro Gly Ala Gly Leu Arg Asp Gln Gln Met Ala Pro Ser Ala Ala Pro  
 180 185 190  
 Gln Ala Pro Glu Ala Phe Thr Leu Lys Glu Lys Gly His Leu Leu Arg  
 195 200 205  
 Leu Pro Ala Ala Phe Arg Lys Ala Ala Ser Gln Asn Ser Ser Leu Trp  
 210 215 220  
 Ala Gln Leu Ser Ser Thr Gln Thr Ser Asp Ser Thr Asp Ala Ala Ala  
 225 230 235 240  
 Ala Lys Thr Gln Phe Leu Gln Asn Met Gln Thr Ala Ser Gly Gly Pro  
 245 250 255  
 Gln Pro Arg Leu Ser Ala Val Glu Val Glu Ala Glu Ala Gly Arg Leu  
 260 265 270  
 Arg Lys Ala Cys Ser Leu Leu Arg Leu Arg Met Arg Glu Glu Leu Ser  
 275 280 285  
 Ala Ala Pro Met Asp Trp Met Gln Glu Tyr Arg Cys Leu Leu Thr Leu  
 290 295 300  
 Glu Gly Leu Gln Ala Met Val Gly Gln Cys Leu His Arg Leu Gln Glu  
 305 310 315 320  
 Leu Arg Ala Ala Val Ala Glu Gln Pro Pro Arg Pro Cys Pro Val Gly  
 325 330 335  
 Arg Pro Pro Gly Ala Ser Pro Ser Cys Gly Gly Arg Ala Glu Pro Ala  
 340 345 350  
 Trp Ser Pro Gln Leu Leu Val Tyr Ser Ser Thr Gln Glu Leu Gln Thr  
 355 360 365  
 Leu Ala Ala Leu Lys Leu Arg Val Ala Val Leu Asp Gln Gln Ile His  
 370 375 380  
 Leu Glu Lys Val Leu Met Ala Glu Leu Leu Pro Leu Val Ser Ala Ala  
 385 390 395 400  
 Gln Pro Gln Gly Pro Pro Trp Leu Ala Leu Cys Arg Ala Val His Ser  
 405 410 415

Leu Leu Cys Glu Gly Gly Ala Arg Val Leu Thr Ile Leu Arg Asp Glu  
420 425 430

Pro Ala Val  
435

<210> 15  
<211> 513  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(510)

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1 5 10 15  
ttc ttg gca ttc att ttc ata ctg gca gct gtg gat act gct gaa gca 96  
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala  
20 25 30  
ggg aag aaa gag aaa cca gaa aaa aaa gtg aag aag tct gac tgt gga 144  
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
35 40 45  
gaa tgg cag tgg agt gtg tgt gtg ccc acc agt gga gac tgt ggg ctg 192  
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu  
50 55 60  
ggc aca cgg gag ggc act cgg act gga gct gag tgc aag caa acc atg 240  
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met  
65 70 75 80  
aag acc cag aga tgt aag atc ccc tgc aac tgg aag aag caa ttt ggc 288  
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly  
85 90 95  
gcg gag tgc aaa tac cag ttc cag gcc tgg gga gaa tgt gac ctg aac 336  
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
100 105 110  
aca gcc ctg aag acc aga act gga agt ctg aag cga gcc ctg cac aat 384

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 115 120 125  
 gcc gaa tgc cag aag act gtc acc atc tcc aag ccc tgt ggc aaa ctg 432  
 Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 130 135 140  
 acc aag ccc aaa cct caa ggt acc cta gaa ctt aaa gta aaa aaa aaa 480  
 Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys  
 145 150 155 160  
 aaa aaa aaa aaa aat tct gag gag acc ttt tag 513  
 Lys Lys Lys Lys Asn Ser Glu Glu Thr Phe  
 165 170

<210> 16  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 20 25 30  
 Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
 35 40 45  
 Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu  
 50 55 60  
 Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met  
 65 70 75 80  
 Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly  
 85 90 95  
 Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 100 105 110  
 Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 115 120 125  
 Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 130 135 140

Thr Lys Pro Lys Pro Gln Gly Thr Leu Glu Leu Lys Val Lys Lys Lys  
 145 150 155 160

Lys Lys Lys Lys Asn Ser Glu Glu Thr Phe  
 165 170

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 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (16)..(297)

<400> 17  
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 gga tca ccc atg tgg cac gtg caa caa ctt gag atc aaa tat gac ttc 99  
 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
 15 20 25  
 cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg acc agc cct 147  
 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
 30 35 40  
 gtg cac cag aag atc tac acc acc ttc atc ctt gtc atc ctc ttc ctc 195  
 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
 45 50 55 60  
 ctg cct ctt atg gaa gaa gaa acg agc tgt cat tat gat ggt gac agt 243  
 Leu Pro Leu Met Glu Glu Glu Thr Ser Cys His Tyr Asp Gly Asp Ser  
 65 70 75  
 ggt ggc tct ctt tgc tgt gtg ctg ggc acc att cca tgt tgt cca tat 291  
 Gly Gly Ser Leu Cys Cys Val Leu Gly Thr Ile Pro Cys Cys Pro Tyr  
 80 85 90  
 gat gat tgaatacagt aattttgaaa aggaatatga tgatgtcaca atcaagatga 347  
 Asp Asp  
 tttttgctat cgtgcaaatt attggatttt ccaactccat ctgtaatccc attgtctatg 407

catttatgaa tgaaaacttc aaaaa

432

<210> 18

<211> 94

<212> PRT

<213> Homo sapiens

<400> 18

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Trp	His	Val	Gln	Gln	Leu	Glu	Ile	Lys	Tyr	Asp	Phe	Leu	Tyr	Glu	Lys
		20						25					30		

Glu	His	Ile	Cys	Cys	Leu	Glu	Glu	Trp	Thr	Ser	Pro	Val	His	Gln	Lys
		35					40					45			

Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Ile	Leu	Phe	Leu	Leu	Pro	Leu	Met
	50					55					60				

Glu	Glu	Glu	Thr	Ser	Cys	His	Tyr	Asp	Gly	Asp	Ser	Gly	Gly	Ser	Leu
65					70					75					80

Cys	Cys	Val	Leu	Gly	Thr	Ile	Pro	Cys	Cys	Pro	Tyr	Asp	Asp
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<210> 19

<211> 1425

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (31)..(1395)

<400> 19

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			Met	Asp	Thr	Pro	Arg	Val	Leu	Leu	
			1					5			

tcg	gcc	gtc	ttc	ctc	atc	agt	ttt	ctg	tgg	gat	ttg	ccc	ggt	ttc	cag	102
Ser	Ala	Val	Phe	Leu	Ile	Ser	Phe	Leu	Trp	Asp	Leu	Pro	Gly	Phe	Gln	
	10					15				20						

cag	gct	tcc	atc	tca	tcc	tcc	tgt	tcg	tcc	gcc	gag	ctg	ggt	tcc	acc	150
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Gln	Ala	Ser	Ile	Ser	Ser	Ser	Cys	Ser	Ser	Ala	Glu	Leu	Gly	Ser	Thr	
25						30				35					40	
aag	ggc	atg	cga	agc	cgc	aag	gaa	ggc	aag	atg	cag	cgg	gcg	ccg	cgc	198
Lys	Gly	Met	Arg	Ser	Arg	Lys	Glu	Gly	Lys	Met	Gln	Arg	Ala	Pro	Arg	
				45					50					55		
gac	agt	gac	gcg	ggc	cgg	gag	ggc	cag	gaa	cca	cag	ccg	cgg	cct	cag	246
Asp	Ser	Asp	Ala	Gly	Arg	Glu	Gly	Gln	Glu	Pro	Gln	Pro	Arg	Pro	Gln	
			60					65					70			
gac	gaa	ccc	cgg	gct	cag	cag	ccc	cgg	gcg	cag	gag	ccg	cca	ggc	agg	294
Asp	Glu	Pro	Arg	Ala	Gln	Gln	Pro	Arg	Ala	Gln	Glu	Pro	Pro	Gly	Arg	
		75					80					85				
ggt	ccg	cgc	gtg	gtg	ccc	cac	gag	tac	atg	ctg	tca	atc	tac	agg	act	342
Gly	Pro	Arg	Val	Val	Pro	His	Glu	Tyr	Met	Leu	Ser	Ile	Tyr	Arg	Thr	
	90					95					100					
tac	tcc	atc	gct	gag	aag	ctg	ggc	atc	aat	gcc	agc	ttt	ttc	cag	tct	390
Tyr	Ser	Ile	Ala	Glu	Lys	Leu	Gly	Ile	Asn	Ala	Ser	Phe	Phe	Gln	Ser	
105					110				115					120		
tcc	aag	tcg	gct	aat	acg	atc	acc	agc	ttt	gta	gac	agg	gga	cta	gac	438
Ser	Lys	Ser	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Val	Asp	Arg	Gly	Leu	Asp	
				125				130					135			
gat	ctc	tcg	cac	act	cct	ctc	cgg	aga	cag	aag	tat	ttg	ttt	gat	gtg	486
Asp	Leu	Ser	His	Thr	Pro	Leu	Arg	Arg	Gln	Lys	Tyr	Leu	Phe	Asp	Val	
			140					145					150			
tcc	atg	ctc	tca	gac	aaa	gaa	gag	ctg	gtg	ggc	gcg	gag	ctg	cgg	ctc	534
Ser	Met	Leu	Ser	Asp	Lys	Glu	Glu	Leu	Val	Gly	Ala	Glu	Leu	Arg	Leu	
		155					160					165				
ttt	cgc	cag	gcg	ccc	tca	gcg	ccc	tgg	ggg	cca	cca	gcc	ggg	ccg	ctc	582
Phe	Arg	Gln	Ala	Pro	Ser	Ala	Pro	Trp	Gly	Pro	Pro	Ala	Gly	Pro	Leu	
	170					175					180					
cac	gtg	cag	ctc	ttc	cct	tgc	ctt	tcg	ccc	cta	ctg	ctg	gac	gcg	cgg	630
His	Val	Gln	Leu	Phe	Pro	Cys	Leu	Ser	Pro	Leu	Leu	Leu	Asp	Ala	Arg	
185					190					195				200		
acc	ctg	gac	ccg	cag	ggg	gcg	ccg	ccg	gcc	ggc	tgg	gaa	gtc	ttc	gac	678
Thr	Leu	Asp	Pro	Gln	Gly	Ala	Pro	Pro	Ala	Gly	Trp	Glu	Val	Phe	Asp	
				205					210					215		
gtg	tgg	cag	ggc	ctg	cgc	cac	cag	ccc	tgg	aag	cag	ctg	tgc	ttg	gag	726



Val	Trp	Gln	Gly	Leu	Arg	His	Gln	Pro	Trp	Lys	Gln	Leu	Cys	Leu	Glu		
			220					225					230				
ctg	cgg	gcc	gca	tgg	ggc	gag	ctg	gac	gcc	ggg	gag	gcc	gag	gcg	cgc	774	
Leu	Arg	Ala	Ala	Trp	Gly	Glu	Leu	Asp	Ala	Gly	Glu	Ala	Glu	Ala	Arg		
		235					240					245					
gcg	cgg	gga	ccc	cag	caa	ccg	ccg	ccc	ccg	gac	ctg	cgg	agt	ctg	ggc	822	
Ala	Arg	Gly	Pro	Gln	Gln	Pro	Pro	Pro	Pro	Asp	Leu	Arg	Ser	Leu	Gly		
		250				255					260						
ttc	ggc	cgg	agg	gtg	cgg	cct	ccc	cag	gag	cgg	gcc	ctg	ctg	gtg	gta	870	
Phe	Gly	Arg	Arg	Val	Arg	Pro	Pro	Gln	Glu	Arg	Ala	Leu	Leu	Val	Val		
265					270				275						280		
ttc	acc	aga	tcc	cag	cgc	aag	aac	ctg	ttc	gca	gag	atg	cgc	gag	cag	918	
Phe	Thr	Arg	Ser	Gln	Arg	Lys	Asn	Leu	Phe	Ala	Glu	Met	Arg	Glu	Gln		
			285					290					295				
ctg	ggc	tcg	gcc	gag	gct	gcg	ggc	ccg	ggc	gcg	ggc	gcc	gag	ggg	tcg	966	
Leu	Gly	Ser	Ala	Glu	Ala	Ala	Gly	Pro	Gly	Ala	Gly	Ala	Glu	Gly	Ser		
			300				305					310					
tgg	ccg	ccg	ccg	tcg	ggc	gcc	ccg	gat	gcc	agg	cct	tgg	ctg	ccc	tcg	1014	
Trp	Pro	Pro	Pro	Ser	Gly	Ala	Pro	Asp	Ala	Arg	Pro	Trp	Leu	Pro	Ser		
		315				320					325						
ccc	ggc	cgc	cgg	cgg	cgg	cgc	acg	gcc	ttc	gcc	agt	cgc	cat	ggc	aag	1062	
Pro	Gly	Arg	Arg	Arg	Arg	Arg	Thr	Ala	Phe	Ala	Ser	Arg	His	Gly	Lys		
		330				335					340						
cgg	cac	ggc	aag	aag	tcc	agg	cta	cgc	tgc	agc	aag	aag	ccc	ctg	cac	1110	
Arg	His	Gly	Lys	Lys	Ser	Arg	Leu	Arg	Cys	Ser	Lys	Lys	Pro	Leu	His		
345					350				355					360			
gtg	aac	ttc	aag	gag	ctg	ggc	tgg	gac	gac	tgg	att	atc	gcg	ccc	ctg	1158	
Val	Asn	Phe	Lys	Glu	Leu	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu		
			365			370							375				
gag	tac	gag	gcc	tat	cac	tgc	gag	ggt	gta	tgc	gac	ttc	ccg	ctg	cgc	1206	
Glu	Tyr	Glu	Ala	Tyr	His	Cys	Glu	Gly	Val	Cys	Asp	Phe	Pro	Leu	Arg		
			380			385						390					
tcg	cac	ctg	gag	ccc	acc	aac	cac	gcc	atc	atc	cag	acg	ctg	atg	aac	1254	
Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Ile	Ile	Gln	Thr	Leu	Met	Asn		
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tcc	atg	gac	ccc	ggc	tcc	acc	ccg	ccc	agc	tgc	tgc	gtg	ccc	acc	aaa	1302	

Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys Cys Val Pro Thr Lys  
 410 415 420

ttg act ccc atc agc att cta tac atc gac gcg ggc aat aat gtg gtc 1350  
 Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala Gly Asn Asn Val Val  
 425 430 435 440

tac aag cag tac gag gac atg gtg gtg gag tcg tgc ggc tgc agg 1395  
 Tyr Lys Gln Tyr Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg  
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<210> 20

<211> 455

<212> PRT

<213> Homo sapiens

<400> 20

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 20 25 30

Ser Ser Ala Glu Leu Gly Ser Thr Lys Gly Met Arg Ser Arg Lys Glu  
 35 40 45

Gly Lys Met Gln Arg Ala Pro Arg Asp Ser Asp Ala Gly Arg Glu Gly  
 50 55 60

Gln Glu Pro Gln Pro Arg Pro Gln Asp Glu Pro Arg Ala Gln Gln Pro  
 65 70 75 80

Arg Ala Gln Glu Pro Pro Gly Arg Gly Pro Arg Val Val Pro His Glu  
 85 90 95

Tyr Met Leu Ser Ile Tyr Arg Thr Tyr Ser Ile Ala Glu Lys Leu Gly  
 100 105 110

Ile Asn Ala Ser Phe Phe Gln Ser Ser Lys Ser Ala Asn Thr Ile Thr  
 115 120 125

Ser Phe Val Asp Arg Gly Leu Asp Asp Leu Ser His Thr Pro Leu Arg  
 130 135 140

Arg Gln Lys Tyr Leu Phe Asp Val Ser Met Leu Ser Asp Lys Glu Glu

145		150		155		160
Leu Val Gly Ala Glu Leu Arg Leu Phe Arg Gln Ala Pro Ser Ala Pro						
	165		170		175	
Trp Gly Pro Pro Ala Gly Pro Leu His Val Gln Leu Phe Pro Cys Leu						
	180		185		190	
Ser Pro Leu Leu Leu Asp Ala Arg Thr Leu Asp Pro Gln Gly Ala Pro						
	195		200		205	
Pro Ala Gly Trp Glu Val Phe Asp Val Trp Gln Gly Leu Arg His Gln						
	210		215		220	
Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala Ala Trp Gly Glu Leu						
225		230		235		240
Asp Ala Gly Glu Ala Glu Ala Arg Ala Arg Gly Pro Gln Gln Pro Pro						
	245		250		255	
Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly Arg Arg Val Arg Pro Pro						
	260		265		270	
Gln Glu Arg Ala Leu Leu Val Val Phe Thr Arg Ser Gln Arg Lys Asn						
	275		280		285	
Leu Phe Ala Glu Met Arg Glu Gln Leu Gly Ser Ala Glu Ala Ala Gly						
	290		295		300	
Pro Gly Ala Gly Ala Glu Gly Ser Trp Pro Pro Pro Ser Gly Ala Pro						
305		310		315		320
Asp Ala Arg Pro Trp Leu Pro Ser Pro Gly Arg Arg Arg Arg Arg Thr						
	325		330		335	
Ala Phe Ala Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu						
	340		345		350	
Arg Cys Ser Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp						
	355		360		365	
Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu						
	370		375		380	
Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His						
385		390		395		400
Ala Ile Ile Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro						

405	410	415
Pro Ser Cys Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr		
420	425	430
Ile Asp Ala Gly Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val		
435	440	445
Val Glu Ser Cys Gly Cys Arg		
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<210> 21  
 <211> 1852  
 <212> DNA  
 <213> Homo sapiens

<400> 21

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ctcagagcag gcgactaaca gacgccaccc tgcaagatga tgtgacaagc acaattatct 1800  
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<210> 22  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:For Ag 390  
 primer

<400> 22  
 accaatgtca tcggaggctt 20

<210> 23  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Rev Ag 390  
 primer

<400> 23  
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<210> 24  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Probe Ag390  
 primer

<400> 24  
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<210> 25  
 <211> 379  
 <212> DNA  
 <213> Homo sapiens

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 atccctagtg gcaaggagac ttccatcgag ctggatgtgc accaccctcc tacagtgacc 300  
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<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Forward Ag 271  
 primer

<400> 26  
 acctggacat agggcgtgtc t 21

<210> 27  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Reverse Ag 271  
 primer

<400> 27  
 tcgatggaag tctccttgcc 20

<210> 28  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Probe Ag 271  
 primer

<400> 28  
 cgaagcatga acgaagccat ccctag 26

<210> 29  
<211> 234  
<212> DNA  
<213> Homo sapiens

<400> 29  
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tcacagcgga aagaccacgc agtggtgacg caacgcccgt tgggacagac tcccgggaag 120  
gactcacact cgttcacatc atcgcagggtg acaccogtca tccgggcaaa gcccgggca 180  
caggcagggt cgatctcgca gcgttcgcag gggctcccc aggctgcccc gagg 234

<210> 30  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Ag 72  
primer

<400> 30  
cggaagacc cagcagtgtt 20

<210> 31  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Ag 72  
primer

<400> 31  
atgatgtgaa cgagtgtgag tcctt 25

<210> 32  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Probe Ag 72  
primer

<400> 32  
cgcccgttgg gacagactcc c

21

<210> 33  
<211> 439  
<212> DNA  
<213> Homo sapiens

<400> 33  
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cacgctgtca cctccttcct ggactggatc cagagcaga tggagagaga cctaaaaacc 300  
tgaagaggaa ggggataagt agccacctga gttcctgagg tgatgaagac agcccgatcc 360  
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cggcaccagt agcaggccc 439

<210> 34  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Ag 248  
primer

<400> 34  
tttccaacaa gatctgcaac ca

22

<210> 35  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse Ag 248  
primer

<400> 35  
aggtagcccg cgcagag

17

<210> 36  
<211> 24



<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Ag 248  
primer

<400> 36  
cgtgtacggt ggcacatctt cccc

24

<210> 37  
<211> 410  
<212> DNA  
<213> Homo sapiens

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cttattgcaa ctcagactgc aattgtgatg aaagtcagtg ggaaccagtc tgtgggaaca 180  
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actcagcgca cttgggtgaa tgcccaagag ataatacttg tacaaggaaa tttttcatct 360  
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<210> 38  
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<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward Ag 287  
primer

<400> 38  
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25

<210> 39  
<211> 28  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Ag 287  
primer

<400> 39  
ctagacaagg tgacaggtaa gttattcc

28

<210> 40  
<211> 27  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:Probe Ag 287  
primer

<400> 40  
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27

<210> 41  
<211> 322  
<212> DNA  
<213> Homo sapiens

<400> 41  
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gcaatgagat ttgtcctccg ga 322

<210> 42  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Ag 252  
primer

<400> 42  
gagctgccgc aactcttcc

19

<210> 43  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Ag 252  
primer

<400> 43

gacaaacttc tctgtgagcg tgtg

24

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Ag 252  
primer

<400> 44

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25

<210> 45

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 45

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<210> 46  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:Forward Ab16  
 Primer

<400> 46  
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<210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Reverse Ab16  
 Primer

<400> 47  
 gcatccgtgg aatcactggt 20

<210> 48  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Probe Ab16  
 Primer

<400> 48  
 tgggcccgag tcagttccac aca 23

<210> 49  
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 <212> DNA  
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<400> 49  
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 aagaccaga gatgtaagat cccctgcaac tggagaagc aatttggcgc ggagtgcaaa 300  
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<210> 50  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:Forward Ag 177  
 Primer

<400> 50  
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<210> 51  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Forward Ag 177  
 Primer

<400> 51  
 tgaggtttgg gcttggtcag 20

<210> 52  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:Forward Ag 177  
 Primer

<400> 52  
caccatctcc aagccctgtg gcaa

24

<210> 53  
<211> 432  
<212> DNA  
<213> Homo sapiens

<400> 53  
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aaattactgt attcaatcat catatggaca acatggaatg gtgccagca cacagcaaag 180  
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ttctaagcag cagatgtgtt ctttttcata taggaagtca tatttgatct caagttgttg 360  
cacgtgccac atgggtgatc ctacgatgac tgccaccagc cagaccacac ctagcattgt 420  
gaaagccctt cg 432

<210> 54  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward GPCR 13  
Primer

<400> 54  
atggaatggt gccagca

18

<210> 55  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Reverse GPCR  
13 Primer

<400> 55  
tggaagaaga aacgagctgt ca

22

<210> 56  
<211> 27

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Probe GPCR 13  
Primer

<400> 56  
cagcaaagag agccaccact gtcacca

27

<210> 57  
<211> 102  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(2)  
<223> Wherein n is a or t or g or c.

<220>  
<221> misc\_feature  
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<223> Wherein n is t or a or g or c.

<400> 57  
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tcggctaata cgatcaccag cttttagac aggggactag nn 102

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Forward Ag 191  
Primer

<400> 58  
gacttactcc atcgctgaga agct

24

<210> 59  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Reverse Ag 191  
Primer

<400> 59

gctggtgac gtattagccg a

21

<210> 60

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Probe Ag 191  
Primer

<400> 60

catcaatgcc agctttttcc agtcttcc

28

<210> 61

<211> 238

<212> DNA

<213> Mus musculus

<220>

<221> misc\_feature

<222> (104)

<223> Wherein n is t or a or g or c.

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<210> 62

<211> 197

<212> DNA

<213> Mus musculus

<400> 62

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cccggtttca cccagca

197

<210> 63

<211> 492

<212> PRT

<213> Homo sapiens

<400> 63

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Val	Pro	Thr	Val	Tyr	Glu	Val	His	Pro	Ala	Gln	Tyr	Tyr	Pro	Ser	Pro
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Val	Pro	Gln	Tyr	Ala	Pro	Arg	Val	Leu	Thr	Gln	Ala	Ser	Asn	Pro	Val
	50					55					60				

Val	Cys	Thr	Gln	Pro	Lys	Ser	Pro	Ser	Gly	Thr	Val	Cys	Thr	Ser	Lys
65					70					75					80

Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val
				85						90				95	

Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys
			100					105						110	

Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
		115						120				125			

Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
	130						135					140			

Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
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Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
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Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn
			180					185					190		

Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
		195					200						205		

Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys	210	215	220	
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Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile	245	250	255	
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	260	265	270	
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	275	280	285	
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	290	295	300	
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met	305	310	315	320
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn	325	330	335	
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	340	345	350	
Lys	Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn	355	360	365	
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Lys	Val	Leu	Leu	Ile	Glu	Thr	Gln	Arg	Cys	Asn	Ser	Arg	Tyr	Val	Tyr	405	410	415	
Asp	Asn	Leu	Ile	Thr	Pro	Ala	Met	Ile	Cys	Ala	Gly	Phe	Leu	Gln	Gly	420	425	430	
Asn	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Thr	Ser	435	440	445	
Asn	Asn	Asn	Ile	Trp	Trp	Leu	Ile	Gly	Asp	Thr	Ser	Trp	Gly	Ser	Gly	450	455	460	

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Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asp Gly  
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<210> 64

<211> 2656

<212> DNA

<213> Homo sapiens

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<210> 65

<211> 1011

<212> PRT

<213> *Drosophila melanogaster*

<400> 65

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Met Ala Leu Arg Gln Ser Ala Lys Asp Val Ala Lys Ser Asn Cys Val
  1              5              10              15

```

```

Ala Val Arg Ser Ser Ile Ser Leu Ser Leu Val Leu Val Leu Cys Leu
      20              25              30

```

```

Ala Leu Val Asp Ser Ser Thr Ala Gln Val Asp Thr Thr Ile Ser Gln
      35              40              45

```

```

Gln Glu Ser Gln Ser Val Val Leu Pro Cys Pro Val Asp Ala Glu Lys
      50              55              60

```

```

Cys Gly Lys Leu His Ser Leu Asn Trp Phe Lys Gly Asp Asp Arg Ile
      65              70              75              80

```

```

Ala Ala Met Leu Leu Gly Asp Ser Asn Val Thr Ser Val Asn Lys Glu
      85              90              95

```

```

Phe Asp Glu Arg Val Thr Val Glu Gln Asn Pro Tyr Arg Leu Val Ile
      100             105             110

```

```

Lys Asp Leu Lys Ile Ala Asp Glu Asp Ile Tyr Leu Cys Asp Thr Thr
      115             120             125

```

```

Phe Phe Ile Pro Glu Glu Thr Cys Asp Asn Phe Asn Gly Tyr Arg Ile
      130             135             140

```

```

Glu Leu Arg Val Leu Val Pro Pro Thr Glu Val Val Ile Leu Asp Ala
      145             150             155             160

```

Lys Gly Asp Arg Ile Lys Asn Gly Ser Val Val Gly Pro Met Gln Glu	165	170	175
Arg Gln Ser Leu Lys Ala Thr Cys Thr Val Arg Asn Thr Arg Pro Gln	180	185	190
Pro Glu Val Ser Trp Phe Arg Gly Thr Lys Arg Leu Thr Thr Tyr Ser	195	200	205
Pro Thr His Asp Leu Val Asp Gly Leu Tyr Thr Ser Thr Leu Glu Leu	210	215	220
Asp Trp Thr Leu Ser Arg Glu Asp Leu Ala Gln Asp Ile Glu Cys Arg	225	230	235
Val Lys Ser Ala Ala Ile Gln Asn Val Thr Val Thr Lys Phe Ser Val	245	250	255
Asp Leu Gln Val Arg Pro Thr Ser Ile Asp Ile Asn Gly Val Lys His	260	265	270
His Thr Val Gln Gly Ser Lys Val Val Leu Thr Cys Asp Ile His Gly	275	280	285
Ala Arg Pro Ala Val Asn Leu Thr Trp Tyr Asn Thr Thr Thr Ile Ile	290	295	300
Ser Ser Gly Glu Asn Glu Ile Thr Glu Val Arg Ser Lys Ser Leu Glu	305	310	315
Lys Ser Asp Gly Thr Phe His Thr Gln Ser Glu Leu Ile Phe Asn Ala	325	330	335
Thr Arg Phe Glu Asn Asp Arg Val Phe Arg Cys Glu Ala Glu Asn Ile	340	345	350
Val Leu Gln Ile Asn Arg Glu Lys Pro Ile Ser Ser Ala Leu Thr Leu	355	360	365
Glu Val Leu Tyr Pro Pro Val Val Lys Val Ser Pro Ser Ala Ile Thr	370	375	380
Ala Asn Thr Ser Glu Ile Val Leu Leu Asn Cys Glu Tyr Phe Ala Asn	385	390	395
Pro Ala Ser Leu Thr Gln Val Glu Trp Tyr Arg Asn Asp Ile Leu Val	405	410	415

Asn Val Asn Asp Thr Thr His Tyr Lys Gly Gly Asn Ser Glu Asn Val	420	425	430
Ala Leu Val Ile Lys Ser Thr Glu Lys Glu Asp Ile Gly Asn Tyr Ser	435	440	445
Cys Gln Leu Ser Asn Asn Ile Gly Lys Gly Thr Ser Asp Gln Lys Ile	450	455	460
Asn Leu Asp Val Gln Tyr Ala Pro Thr Val Glu Ile Leu Met Ile Pro	465	470	475
Glu Gly Pro Val Lys Glu Ser Asp Glu Ser Asn Val Thr Leu Phe Cys	485	490	495
Asn Val Leu Asp Ala Asn Pro Ser Val Leu Thr Lys Val Arg Trp Tyr	500	505	510
Ala Asn Ser Thr Leu Leu Lys Glu Leu Pro Asp Cys Glu Glu Thr Arg	515	520	525
Glu Asp Leu Cys His Ile Asp Pro Ser Lys Leu Leu Leu Glu Ser Ile	530	535	540
Gly Arg Gly Phe Phe Tyr Asn Tyr Ser Cys Glu Gly Phe Asn Ala Ala	545	550	555
Gly Trp Gly Pro Arg Ser Glu Asp Lys Glu Leu Leu Val His Tyr Glu	565	570	575
Pro Gly Pro Ala Ala Leu Ser His Phe Pro Leu Val Ala Val Lys Lys	580	585	590
Lys Ser Val Thr Phe Ser Cys Ser Val Asp Asp Pro Gly Phe Pro Glu	595	600	605
Ser Asn Arg Phe Arg Trp Leu Arg Gly Gly Arg Gly Pro Leu Gln Asp	610	615	620
Ile Val Thr Lys Asp Trp Thr Val Glu Pro Val Gly Leu Asp Ser Arg	625	630	635
Thr Asn Tyr Ser Cys Tyr Ala Tyr Asn Glu Gly Gly Lys Gly Val Met	645	650	655
Ala Thr Val Asn Leu Glu Val His Ala Pro Pro Phe Phe Ile Lys Asn	660	665	670

Leu Pro Pro Tyr Thr Gly Ile Leu His Ser Ser Pro Asn Ala Thr Leu  
 675 680 685  
 Thr Cys Arg Ile Glu Cys Val Pro Arg Cys Asp Ile Ser Trp Gln Lys  
 690 695 700  
 Asp Gly Val Pro Ile Glu Arg Asn Asp Ser Arg Tyr Phe Ile Lys Glu  
 705 710 715 720  
 Asn Thr Trp Met Pro Pro Pro Gln Arg Glu Ile Leu Lys Ser Met Leu  
 725 730 735  
 Ser Val Leu His Phe Asn Met Pro Asn Trp Pro Asp Ser Lys Phe Asn  
 740 745 750  
 Ile Glu Ala Asp Asn Ala Asn Tyr Ser Cys Val Ser Thr Gly Asn Ile  
 755 760 765  
 Val Gly Gly Ser Ile Arg Ser Arg Thr Tyr Tyr Phe Gly Ile Glu Ala  
 770 775 780  
 Pro Glu Asn Thr Thr Val Ser Glu Asn Ile Val Tyr Val Gln Glu Asp  
 785 790 795 800  
 Thr Ile Pro Gly Arg Val Ile Cys Lys Ser Arg Ala Asn Pro Glu Pro  
 805 810 815  
 Ser Tyr Lys Trp Ile Phe Lys Asn Glu Thr Ile Ala Asn Gly Asn Ala  
 820 825 830  
 Leu Ile Ile Asn Thr Ala Met Asn Arg Asn Asp Asp Gly Thr Tyr Thr  
 835 840 845  
 Cys Leu Ala Tyr Asn Lys His Gly Ser Ser Ile Ala Lys Thr Val Ile  
 850 855 860  
 Lys Val Gln Phe Lys Pro Arg Cys Glu Ile Glu Arg Gln Glu Ile Asp  
 865 870 875 880  
 Asp Gln Asp Thr Leu Ile Cys Thr Ala Tyr Gly Asn Pro Ile Glu Ala  
 885 890 895  
 Asp Phe Ser Trp Ser Ile Lys Thr Glu Asn Glu Thr Asp Glu Asn Leu  
 900 905 910  
 Gly Ser Gly Lys Lys Glu Asn Ser Val Glu Lys Ser Phe Tyr Ile Leu  
 915 920 925

Gln Thr Asp Tyr Ala Ile Ser Arg Thr Tyr Arg Cys Val Ala Asn Asn  
 930 935 940

Thr Val Gly Tyr Gly Pro Phe Cys Glu Ile Glu Val Ala Glu Gln Leu  
 945 950 955 960

Ala Trp Trp Gln Leu Trp Glu Lys Asn Thr Leu Ile Ile Leu Val Ala  
 965 970 975

Ala Ile Leu Gly Leu Leu Leu Thr Val Ile Val Ile Cys Cys Ile Ile  
 980 985 990

Ile Cys Ile Cys Arg Pro Val Gly Ala Arg Ile Asn Tyr Thr Thr Ser  
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Arg Leu His  
 1010

<210> 66  
 <211> 862  
 <212> PRT  
 <213> Mus musculus

<400> 66  
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Ser Ala Gln Tyr Ser Ser Ala Asn Asp Trp Thr Val Asp His Pro Gln  
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Thr Leu Phe Ala Trp Glu Gly Ala Cys Ile Arg Ile Pro Cys Lys Tyr  
 35 40 45

Lys Thr Pro Leu Pro Lys Ala Arg Leu Asp Asn Ile Leu Leu Phe Gln  
 50 55 60

Asn Tyr Glu Phe Asp Lys Ala Thr Lys Lys Phe Lys Gly Thr Val Leu  
 65 70 75 80

Tyr Asn Lys Ala Glu Pro Glu Leu Tyr Pro Pro Lys Gln Arg Arg Val  
 85 90 95

Thr Phe Leu Gly Asn Ser Ile Asp Asn Cys Thr Leu Lys Ile His Pro  
 100 105 110

Ile Arg Ala Asn Asp Ser Gly Asn Leu Gly Leu Arg Met Thr Ala Gly  
 115 120 125



Thr	Glu	Arg	Trp	Met	Glu	Pro	Ile	His	Leu	Asn	Val	Ser	Glu	Lys	Pro	130	135	140
Phe	Gln	Pro	Tyr	Ile	Gln	Met	Pro	Ser	Glu	Ile	Arg	Glu	Ser	Gln	Ser	145	150	155 160
Val	Thr	Leu	Thr	Cys	Gly	Leu	Asn	Phe	Ser	Cys	Phe	Glu	Tyr	Asp	Ile	165	170	175
Leu	Leu	Gln	Trp	Phe	Leu	Glu	Asp	Ser	Lys	Ile	Thr	Ser	Val	Thr	Pro	180	185	190
Ser	Val	Thr	Ser	Ile	Thr	Ser	Ser	Val	Thr	Ser	Ser	Ile	Lys	Asn	Val	195	200	205
Tyr	Thr	Glu	Ser	Lys	Leu	Thr	Phe	Gln	Pro	Lys	Trp	Thr	Asp	His	Gly	210	215	220
Lys	Ser	Val	Lys	Cys	Gln	Val	Gln	His	Ser	Ser	Glu	Val	Leu	Ser	Glu	225	230	235 240
Arg	Thr	Val	Arg	Leu	Asp	Val	Lys	Tyr	Thr	Pro	Lys	Leu	Glu	Ile	Lys	245	250	255
Val	Asn	Pro	Thr	Glu	Val	Glu	Lys	Asn	Asn	Ser	Val	Thr	Met	Thr	Cys	260	265	270
Arg	Val	Asn	Ser	Ser	Asn	Pro	Lys	Leu	Arg	Thr	Val	Ala	Val	Ser	Trp	275	280	285
Phe	Lys	Asp	Gly	Arg	Pro	Leu	Glu	Asp	Gln	Glu	Leu	Glu	Gln	Glu	Gln	290	295	300
Gln	Met	Ser	Lys	Leu	Ile	Leu	His	Ser	Val	Thr	Lys	Asp	Met	Arg	Gly	305	310	315 320
Lys	Tyr	Arg	Cys	Gln	Ala	Ser	Asn	Asp	Ile	Gly	Pro	Gly	Glu	Ser	Glu	325	330	335
Glu	Val	Glu	Leu	Thr	Val	His	Tyr	Ala	Pro	Glu	Pro	Ser	Arg	Val	His	340	345	350
Ile	Tyr	Pro	Ser	Pro	Ala	Glu	Glu	Gly	Gln	Ser	Val	Glu	Leu	Ile	Cys	355	360	365
Glu	Ser	Leu	Ala	Ser	Pro	Ser	Ala	Thr	Asn	Tyr	Thr	Trp	Tyr	His	Asn	370	375	380

Arg Lys Pro Ile Pro Gly Asp Thr Gln Glu Lys Leu Arg Ile Pro Lys  
 385 390 395 400

Val Ser Pro Trp His Ala Gly Asn Tyr Ser Cys Leu Ala Glu Asn Arg  
 405 410 415

Leu Gly His Gly Lys Ile Asp Gln Glu Ala Lys Leu Asp Val His Tyr  
 420 425 430

Ala Pro Lys Ala Val Thr Thr Val Ile Gln Ser Phe Thr Pro Ile Leu  
 435 440 445

Glu Gly Asp Ser Val Thr Leu Val Cys Arg Tyr Asn Ser Ser Asn Pro  
 450 455 460

Asp Val Thr Ser Tyr Arg Trp Asn Pro Gln Gly Ser Gly Ser Val Leu  
 465 470 475 480

Lys Pro Gly Val Leu Arg Ile Gln Lys Val Thr Trp Asp Ser Met Pro  
 485 490 495

Val Ser Cys Ala Ala Cys Asn His Lys Cys Ser Trp Ala Leu Pro Val  
 500 505 510

Ile Leu Asn Val His Tyr Ala Pro Arg Asp Val Lys Val Leu Lys Val  
 515 520 525

Ser Pro Ala Ser Glu Ile Arg Ala Gly Gln Arg Val Leu Leu Gln Cys  
 530 535 540

Asp Phe Ala Glu Ser Asn Pro Ala Glu Val Arg Phe Phe Trp Lys Lys  
 545 550 555 560

Asn Gly Ser Leu Val Gln Glu Gly Arg Tyr Leu Ser Phe Gly Ser Val  
 565 570 575

Ser Pro Glu Asp Ser Gly Asn Tyr Asn Cys Met Val Asn Asn Ser Ile  
 580 585 590

Gly Glu Thr Leu Ser Gln Ala Trp Asn Leu Gln Val Leu Tyr Ala Pro  
 595 600 605

Arg Arg Leu Arg Val Ser Ile Ser Pro Gly Asp His Val Met Glu Gly  
 610 615 620

Lys Lys Ala Thr Leu Ser Cys Glu Ser Asp Ala Asn Pro Pro Ile Ser  
 625 630 635 640

Gln Tyr Thr Trp Phe Asp Ser Ser Gly Gln Asp Leu His Ser Ser Gly	645	650	655
Gln Lys Leu Arg Leu Glu Pro Leu Glu Val Gln His Thr Gly Ser Tyr	660	665	670
Arg Cys Lys Gly Thr Asn Gly Ile Gly Thr Gly Glu Ser Pro Pro Ser	675	680	685
Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Lys Arg Val Ala	690	695	700
Leu Gly Leu Gly Phe Cys Leu Thr Ile Cys Ile Leu Ala Ile Trp Gly	705	710	715
Met Lys Ile Gln Lys Lys Trp Lys Gln Asn Arg Ser Gln Gln Gly Leu	725	730	735
Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys Ala	740	745	750
Arg Arg Thr Pro Leu Ser Glu Gly Pro Gln Ser Gln Gly Cys Tyr Asn	755	760	765
Pro Ala Met Asp Asp Thr Val Ser Tyr Ala Ile Leu Arg Phe Pro Glu	770	775	780
Ser Asp Met His Asn Ala Gly Asp Ala Gly Thr Pro Ala Thr Gln Ala	785	790	795
Pro Pro Pro Asn Asn Ser Asp Ser Val Thr Tyr Ser Val Ile Gln Lys	805	810	815
Arg Pro Met Gly Asp Tyr Glu Asn Val Asn Pro Ser Cys Pro Glu Asp	820	825	830
Glu Ser Ile His Tyr Ser Glu Leu Val Gln Phe Gly Ala Gly Lys Arg	835	840	845
Pro Gln Ala Lys Glu Asp Val Asp Tyr Val Thr Leu Lys His	850	855	860

<210> 67

<211> 1399

<212> DNA

<213> Homo sapiens

<400> 67

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cagggagccc tcttttcttg gagctcacag cctaacagga agacagacat gaataacatg 780
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<210> 68

<211> 2911

<212> PRT

<213> Homo sapiens

<400> 68

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Gly Cys Val Val Leu Trp Ala Gln Gly Thr Ala Gly Gln Pro Gln Pro
      20              25              30

Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg
      35              40              45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg
      50              55              60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Arg Gly Gln Gln
      65              70              75              80
```

Asp	Val	Leu	Arg	Gly	Pro	Asn	Val	Cys	Gly	Ser	Arg	Phe	His	Ser	Tyr	85	90	95
Cys	Cys	Pro	Gly	Trp	Lys	Thr	Leu	Pro	Gly	Gly	Asn	Gln	Cys	Ile	Val	100	105	110
Pro	Ile	Cys	Arg	Asn	Ser	Cys	Gly	Asp	Gly	Phe	Cys	Ser	Arg	Pro	Asn	115	120	125
Met	Cys	Thr	Cys	Ser	Ser	Gly	Gln	Ile	Ser	Ser	Thr	Cys	Gly	Ser	Lys	130	135	140
Ser	Ile	Gln	Gln	Cys	Ser	Val	Arg	Cys	Met	Asn	Gly	Gly	Thr	Cys	Ala	145	150	155
Asp	Asp	His	Cys	Gln	Cys	Gln	Lys	Gly	Tyr	Ile	Gly	Thr	Tyr	Cys	Gly	165	170	175
Gln	Pro	Val	Cys	Glu	Asn	Gly	Cys	Gln	Asn	Gly	Gly	Arg	Cys	Ile	Ala	180	185	190
Gln	Pro	Cys	Ala	Cys	Val	Tyr	Gly	Phe	Thr	Gly	Pro	Gln	Cys	Glu	Arg	195	200	205
Asp	Tyr	Arg	Thr	Gly	Pro	Cys	Phe	Thr	Gln	Val	Asn	Asn	Gln	Met	Cys	210	215	220
Gln	Gly	Gln	Leu	Thr	Gly	Ile	Val	Cys	Thr	Lys	Thr	Leu	Cys	Cys	Ala	225	230	235
Thr	Thr	Gly	Arg	Ala	Trp	Gly	His	Pro	Cys	Glu	Met	Cys	Pro	Ala	Gln	245	250	255
Pro	Gln	Pro	Cys	Arg	Arg	Gly	Phe	Ile	Pro	Asn	Ile	Arg	Thr	Gly	Ala	260	265	270
Cys	Gln	Asp	Val	Asp	Glu	Cys	Gln	Ala	Ile	Pro	Gly	Ile	Cys	Gln	Gly	275	280	285
Gly	Asn	Cys	Ile	Asn	Thr	Val	Gly	Ser	Phe	Glu	Cys	Arg	Cys	Pro	Ala	290	295	300
Gly	His	Lys	Gln	Ser	Glu	Thr	Thr	Gln	Lys	Cys	Glu	Asp	Ile	Asp	Glu	305	310	315
Cys	Ser	Ile	Ile	Pro	Gly	Ile	Cys	Glu	Thr	Gly	Glu	Cys	Ser	Asn	Thr	325	330	335

Val Gly Ser Tyr Phe Cys Val Cys Pro Arg Gly Tyr Val Thr Ser Thr	340	345	350
Asp Gly Ser Arg Cys Ile Asp Gln Arg Thr Gly Met Cys Phe Ser Gly	355	360	365
Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr Lys	370	375	380
Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr Ile	385	390	395
Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu Cys	405	410	415
Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser Arg	420	425	430
Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly Asn	435	440	445
Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly Asn	450	455	460
Gly Phe Ser Pro Gly Val Gly Gly Ala Gly Val Gly Ala Gly Gly Gln	465	470	475
Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp Ile	485	490	495
Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro Thr	500	505	510
Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp Ala	515	520	525
Asn Gly Asp Cys Ile Asp Val Asp Glu Cys Thr Ser Asn Pro Cys Thr	530	535	540
Asn Gly Asp Cys Val Asn Thr Pro Gly Ser Tyr Tyr Cys Lys Cys His	545	550	555
Ala Gly Phe Gln Arg Thr Pro Thr Lys Gln Ala Cys Ile Asp Ile Asp	565	570	575
Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val Asn	580	585	590

Ser	Asp	Gly	Ser	Phe	Gln	Cys	Ile	Cys	Asn	Ala	Gly	Phe	Glu	Leu	Thr	595	600	605	
Thr	Asp	Gly	Lys	Asn	Cys	Val	Asp	His	Asp	Glu	Cys	Thr	Thr	Thr	Asn	610	615	620	
Met	Cys	Leu	Asn	Gly	Met	Cys	Ile	Asn	Glu	Asp	Gly	Ser	Phe	Lys	Cys	625	630	635	640
Ile	Cys	Lys	Pro	Gly	Phe	Val	Leu	Ala	Pro	Asn	Gly	Arg	Tyr	Cys	Thr	645	650	655	
Asp	Val	Asp	Glu	Cys	Gln	Thr	Pro	Gly	Ile	Cys	Met	Asn	Gly	His	Cys	660	665	670	
Ile	Asn	Ser	Glu	Gly	Ser	Phe	Arg	Cys	Asp	Cys	Pro	Pro	Gly	Leu	Ala	675	680	685	
Val	Gly	Met	Asp	Gly	Arg	Val	Cys	Val	Asp	Thr	His	Met	Arg	Ser	Thr	690	695	700	
Cys	Tyr	Gly	Gly	Ile	Lys	Lys	Gly	Val	Cys	Val	Arg	Pro	Phe	Pro	Gly	705	710	715	720
Ala	Val	Thr	Lys	Ser	Glu	Cys	Cys	Cys	Ala	Asn	Pro	Asp	Tyr	Gly	Phe	725	730	735	
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Asn	Glu	Cys	Ala	Leu	Asp	Pro	Asp	Ile	Cys	Ala	Asn	Gly	Ile	Cys	Glu	770	775	780	
Asn	Leu	Arg	Gly	Ser	Tyr	Arg	Cys	Asn	Cys	Asn	Ser	Gly	Tyr	Glu	Pro	785	790	795	800
Asp	Ala	Ser	Gly	Arg	Asn	Cys	Ile	Asp	Ile	Asp	Glu	Cys	Leu	Val	Asn	805	810	815	
Arg	Leu	Leu	Cys	Asp	Asn	Gly	Leu	Cys	Arg	Asn	Thr	Pro	Gly	Ser	Tyr	820	825	830	
Ser	Cys	Thr	Cys	Pro	Pro	Gly	Tyr	Val	Phe	Arg	Thr	Glu	Thr	Glu	Thr	835	840	845	

Cys Glu Asp Ile Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Ala  
850 855 860  
Cys Arg Asn Asn Leu Gly Ser Phe Asn Cys Glu Cys Ser Pro Gly Ser  
865 870 875 880  
Lys Leu Ser Ser Thr Gly Leu Ile Cys Ile Asp Ser Leu Lys Gly Thr  
885 890 895  
Cys Trp Leu Asn Ile Gln Asp Ser Arg Cys Glu Val Asn Ile Asn Gly  
900 905 910  
Ala Thr Leu Lys Ser Glu Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly  
915 920 925  
Ser Pro Cys Glu Arg Cys Glu Leu Asp Thr Ala Cys Pro Arg Gly Leu  
930 935 940  
Ala Arg Ile Lys Gly Val Thr Cys Glu Asp Val Asn Glu Cys Glu Val  
945 950 955 960  
Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Ser Lys Gly Ser  
965 970 975  
Phe His Cys Glu Cys Pro Glu Gly Leu Thr Leu Asp Gly Thr Gly Arg  
980 985 990  
Val Cys Leu Asp Ile Arg Met Glu Gln Cys Tyr Leu Lys Trp Asp Glu  
995 1000 1005  
Asp Glu Cys Ile His Pro Val Pro Gly Lys Phe Arg Met Asp Ala Cys  
1010 1015 1020  
Cys Cys Ala Val Gly Ala Ala Trp Gly Thr Glu Cys Glu Glu Cys Pro  
1025 1030 1035 1040  
Lys Pro Gly Thr Lys Glu Tyr Glu Thr Leu Cys Pro Arg Gly Ala Gly  
1045 1050 1055  
Phe Ala Asn Arg Gly Asp Val Leu Thr Gly Arg Pro Phe Tyr Lys Asp  
1060 1065 1070  
Ile Asn Glu Cys Lys Ala Phe Pro Gly Met Cys Thr Tyr Gly Lys Cys  
1075 1080 1085  
Arg Asn Thr Ile Gly Ser Phe Lys Cys Arg Cys Asn Ser Gly Phe Ala  
1090 1095 1100



Leu Asp Met Glu Glu Arg Asn Cys Thr Asp Ile Asp Glu Cys Arg Ile			
1105	1110	1115	1120
Ser Pro Asp Leu Cys Gly Ser Gly Ile Cys Val Asn Thr Pro Gly Ser			
1125	1130	1135	
Phe Glu Cys Glu Cys Phe Glu Gly Tyr Glu Ser Gly Phe Met Met Met			
1140	1145	1150	
Lys Asn Cys Met Asp Ile Asp Gly Cys Glu Arg Asn Pro Leu Leu Cys			
1155	1160	1165	
Arg Gly Gly Thr Cys Val Asn Thr Glu Gly Ser Phe Gln Cys Asp Cys			
1170	1175	1180	
Pro Leu Gly His Glu Leu Ser Pro Ser Arg Glu Asp Cys Val Asp Ile			
1185	1190	1195	1200
Asn Glu Cys Ser Leu Ser Asp Asn Leu Cys Arg Asn Gly Lys Cys Val			
1205	1210	1215	
Asn Met Ile Gly Thr Tyr Gln Cys Ser Cys Asn Pro Gly Tyr Gln Ala			
1220	1225	1230	
Thr Pro Asp Arg Gln Gly Cys Thr Asp Ile Asp Glu Cys Met Ile Met			
1235	1240	1245	
Asn Gly Gly Cys Asp Thr Gln Cys Thr Asn Ser Glu Gly Ser Tyr Glu			
1250	1255	1260	
Cys Ser Cys Ser Glu Gly Tyr Ala Leu Met Pro Asp Gly Arg Ser Cys			
1265	1270	1275	1280
Ala Asp Ile Asp Glu Cys Glu Asn Asn Pro Asp Ile Cys Asp Gly Gly			
1285	1290	1295	
Gln Cys Thr Asn Ile Pro Gly Glu Tyr Arg Cys Leu Cys Tyr Asp Gly			
1300	1305	1310	
Phe Met Ala Ser Met Asp Met Lys Thr Cys Ile Asp Val Asn Glu Cys			
1315	1320	1325	
Asp Leu Asn Ser Asn Ile Cys Met Phe Gly Glu Cys Glu Asn Thr Lys			
1330	1335	1340	
Gly Ser Phe Ile Cys His Cys Gln Leu Gly Tyr Ser Val Lys Lys Gly			
1345	1350	1355	1360

Thr Thr Gly Cys Thr Asp Val Asp Glu Cys Glu Ile Gly Ala His Asn		
1365	1370	1375
Cys Asp Met His Ala Ser Cys Leu Asn Ile Pro Gly Ser Phe Lys Cys		
1380	1385	1390
Ser Cys Arg Glu Gly Trp Ile Gly Asn Gly Ile Lys Cys Ile Asp Leu		
1395	1400	1405
Asp Glu Cys Ser Asn Gly Thr His Gln Cys Ser Ile Asn Ala Gln Cys		
1410	1415	1420
Val Asn Thr Pro Gly Ser Tyr Arg Cys Ala Cys Ser Glu Gly Phe Thr		
1425	1430	1435
Gly Asp Gly Phe Thr Cys Ser Asp Val Asp Glu Cys Ala Glu Asn Ile		
1445	1450	1455
Asn Leu Cys Glu Asn Gly Gln Cys Leu Asn Val Pro Gly Ala Tyr Arg		
1460	1465	1470
Cys Glu Cys Glu Met Gly Phe Thr Pro Ala Ser Asp Ser Arg Ser Cys		
1475	1480	1485
Gln Asp Ile Asp Glu Cys Ser Phe Gln Asn Ile Cys Val Ser Gly Thr		
1490	1495	1500
Cys Asn Asn Leu Pro Gly Met Phe His Cys Ile Cys Asp Asp Gly Tyr		
1505	1510	1515
Glu Leu Asp Arg Thr Gly Gly Asn Cys Thr Asp Ile Asp Glu Cys Ala		
1525	1530	1535
Asp Pro Ile Asn Cys Val Asn Gly Leu Cys Val Asn Thr Pro Gly Arg		
1540	1545	1550
Tyr Glu Cys Asn Cys Pro Pro Asp Phe Gln Leu Asn Pro Thr Gly Val		
1555	1560	1565
Gly Cys Val Asp Asn Arg Val Gly Asn Cys Tyr Leu Lys Phe Gly Pro		
1570	1575	1580
Arg Gly Asp Gly Ser Leu Ser Cys Asn Thr Glu Ile Gly Val Gly Val		
1585	1590	1595
Ser Arg Ser Ser Cys Cys Cys Ser Leu Gly Lys Ala Trp Gly Asn Pro		
1605	1610	1615

Cys Glu Thr Cys Pro Pro Val Asn Ser Thr Glu Tyr Tyr Thr Leu Cys	1620	1625	1630
Pro Gly Gly Glu Gly Phe Arg Pro Asn Pro Ile Thr Ile Ile Leu Glu	1635	1640	1645
Asp Ile Asp Glu Cys Gln Glu Leu Pro Gly Leu Cys Gln Gly Gly Asn	1650	1655	1660
Cys Ile Asn Thr Phe Gly Ser Phe Gln Cys Glu Cys Pro Gln Gly Tyr	1665	1670	1675
Tyr Leu Ser Glu Asp Thr Arg Ile Cys Glu Asp Ile Asp Glu Cys Phe	1685	1690	1695
Ala His Pro Gly Val Cys Gly Pro Gly Thr Cys Tyr Asn Thr Leu Gly	1700	1705	1710
Asn Tyr Thr Cys Ile Cys Pro Pro Glu Tyr Met Gln Val Asn Gly Gly	1715	1720	1725
His Asn Cys Met Asp Met Arg Lys Ser Phe Cys Tyr Arg Ser Tyr Asn	1730	1735	1740
Gly Thr Thr Cys Glu Asn Glu Leu Pro Phe Asn Val Thr Lys Arg Met	1745	1750	1755
Cys Cys Cys Thr Tyr Asn Val Gly Lys Ala Gly Asn Lys Pro Cys Glu	1765	1770	1775
Pro Cys Pro Thr Pro Gly Thr Ala Asp Phe Lys Thr Ile Cys Gly Asn	1780	1785	1790
Ile Pro Gly Phe Thr Phe Asp Ile His Thr Gly Lys Ala Val Asp Ile	1795	1800	1805
Asp Glu Cys Lys Glu Ile Pro Gly Ile Cys Ala Asn Gly Val Cys Ile	1810	1815	1820
Asn Gln Ile Gly Ser Phe Arg Cys Glu Cys Pro Thr Gly Phe Ser Tyr	1825	1830	1835
Asn Asp Leu Leu Leu Val Cys Glu Asp Ile Asp Glu Cys Ser Asn Gly	1845	1850	1855
Asp Asn Leu Cys Gln Arg Asn Ala Asp Cys Ile Asn Ser Pro Gly Ser	1860	1865	1870

Tyr Arg Cys Glu Cys Ala Ala Gly Phe Lys Leu Ser Pro Asn Gly Ala		
1875	1880	1885
Cys Val Asp Arg Asn Glu Cys Leu Glu Ile Pro Asn Val Cys Ser His		
1890	1895	1900
Gly Leu Cys Val Asp Leu Gln Gly Ser Tyr Gln Cys Ile Cys His Asn		
1905	1910	1915 1920
Gly Phe Lys Ala Ser Gln Asp Gln Thr Met Cys Met Asp Val Asp Glu		
	1925	1930 1935
Cys Glu Arg His Pro Cys Gly Asn Gly Thr Cys Lys Asn Thr Val Gly		
	1940	1945 1950
Ser Tyr Asn Cys Leu Cys Tyr Pro Gly Phe Glu Leu Thr His Asn Asn		
	1955	1960 1965
Asp Cys Leu Asp Ile Asp Glu Cys Ser Ser Phe Phe Gly Gln Val Cys		
	1970	1975 1980
Arg Asn Gly Arg Cys Phe Asn Glu Ile Gly Ser Phe Lys Cys Leu Cys		
	1985	1990 1995 2000
Asn Glu Gly Tyr Glu Leu Thr Pro Asp Gly Lys Asn Cys Ile Asp Thr		
	2005	2010 2015
Asn Glu Cys Val Ala Leu Pro Gly Ser Cys Ser Pro Gly Thr Cys Gln		
	2020	2025 2030
Asn Leu Glu Gly Ser Phe Arg Cys Ile Cys Pro Pro Gly Tyr Glu Val		
	2035	2040 2045
Lys Ser Glu Asn Cys Ile Asp Ile Asn Glu Cys Asp Glu Asp Pro Asn		
	2050	2055 2060
Ile Cys Leu Phe Gly Ser Cys Thr Asn Thr Pro Gly Gly Phe Gln Cys		
	2065	2070 2075 2080
Leu Cys Pro Pro Gly Phe Val Leu Ser Asp Asn Gly Arg Arg Cys Phe		
	2085	2090 2095
Asp Thr Arg Gln Ser Phe Cys Phe Thr Asn Phe Glu Asn Gly Lys Cys		
	2100	2105 2110
Ser Val Pro Lys Ala Phe Asn Thr Thr Lys Ala Lys Cys Cys Cys Ser		
	2115	2120 2125

Lys Met Pro Gly Glu Gly Trp Gly Asp Pro Cys Glu Leu Cys Pro Lys  
 2130 2135 2140

Asp Asp Glu Val Ala Phe Gln Asp Leu Cys Pro Tyr Gly His Gly Thr  
 2145 2150 2155 2160

Val Pro Ser Leu His Asp Thr Arg Glu Asp Val Asn Glu Cys Leu Glu  
 2165 2170 2175

Ser Pro Gly Ile Cys Ser Asn Gly Gln Cys Ile Asn Thr Asp Gly Ser  
 2180 2185 2190

Phe Arg Cys Glu Cys Pro Met Gly Tyr Asn Leu Asp Tyr Thr Gly Val  
 2195 2200 2205

Arg Cys Val Asp Thr Asp Glu Cys Ser Ile Gly Asn Pro Cys Gly Asn  
 2210 2215 2220

Gly Thr Cys Thr Asn Val Ile Gly Ser Phe Glu Cys Asn Cys Asn Glu  
 2225 2230 2235 2240

Gly Phe Glu Pro Gly Pro Met Met Asn Cys Glu Asp Ile Asn Glu Cys  
 2245 2250 2255

Ala Gln Asn Pro Leu Leu Cys Ala Leu Arg Cys Met Asn Thr Phe Gly  
 2260 2265 2270

Ser Tyr Glu Cys Thr Cys Pro Ile Gly Tyr Ala Leu Arg Glu Asp Gln  
 2275 2280 2285

Lys Met Cys Lys Asp Leu Asp Glu Cys Ala Glu Gly Leu His Asp Cys  
 2290 2295 2300

Glu Ser Arg Gly Met Met Cys Lys Asn Leu Ile Gly Thr Phe Met Cys  
 2305 2310 2315 2320

Ile Cys Pro Pro Gly Met Ala Arg Arg Pro Asp Gly Glu Gly Cys Val  
 2325 2330 2335

Asp Glu Asn Glu Cys Arg Thr Lys Pro Gly Ile Cys Glu Asn Gly Arg  
 2340 2345 2350

Cys Val Asn Ile Ile Gly Ser Tyr Arg Cys Glu Cys Asn Glu Gly Phe  
 2355 2360 2365

Gln Ser Ser Ser Ser Gly Thr Glu Cys Leu Asp Asn Arg Gln Gly Leu  
 2370 2375 2380

Cys Phe Ala Glu Val Leu Gln Thr Ile Cys Gln Met Ala Ser Ser Ser  
 2385                      2390                      2395                      2400

Arg Asn Leu Val Thr Lys Ser Glu Cys Cys Cys Asp Gly Gly Arg Gly  
                     2405                      2410                      2415

Trp Gly His Gln Cys Glu Leu Cys Pro Leu Pro Gly Thr Ala Gln Tyr  
                     2420                      2425                      2430

Lys Lys Ile Cys Pro His Gly Pro Gly Tyr Thr Thr Asp Gly Arg Asp  
                     2435                      2440                      2445

Ile Asp Glu Cys Lys Val Met Pro Asn Leu Cys Thr Asn Gly Gln Cys  
                     2450                      2455                      2460

Ile Asn Thr Met Gly Ser Phe Arg Cys Phe Cys Lys Val Gly Tyr Thr  
 2465                      2470                      2475                      2480

Thr Asp Ile Ser Gly Thr Ser Cys Ile Asp Leu Asp Glu Cys Ser Gln  
                     2485                      2490                      2495

Ser Pro Lys Pro Cys Asn Tyr Ile Cys Lys Asn Thr Glu Gly Ser Tyr  
                     2500                      2505                      2510

Gln Cys Ser Cys Pro Arg Gly Tyr Val Leu Gln Glu Asp Gly Lys Thr  
                     2515                      2520                      2525

Cys Lys Asp Leu Asp Glu Cys Gln Thr Lys Gln His Asn Cys Gln Phe  
                     2530                      2535                      2540

Leu Cys Val Asn Thr Leu Gly Gly Phe Thr Cys Lys Cys Pro Pro Gly  
 2545                      2550                      2555                      2560

Phe Thr Gln His His Thr Ala Cys Ile Asp Asn Asn Glu Cys Gly Ser  
                     2565                      2570                      2575

Gln Pro Leu Leu Cys Gly Gly Lys Gly Ile Cys Gln Asn Thr Pro Gly  
                     2580                      2585                      2590

Ser Phe Ser Cys Glu Cys Gln Arg Gly Phe Ser Leu Asp Ala Thr Gly  
                     2595                      2600                      2605

Leu Asn Cys Glu Asp Val Asp Glu Cys Asp Gly Asn His Arg Cys Gln  
                     2610                      2615                      2620

His Gly Cys Gln Asn Ile Leu Gly Gly Tyr Arg Cys Gly Cys Pro Gln  
 2625                      2630                      2635                      2640

Gly Tyr Ile Gln His Tyr Gln Trp Asn Gln Cys Val Asp Glu Asn Glu  
 2645 2650 2655  
 Cys Ser Asn Pro Asn Ala Cys Gly Ser Ala Ser Cys Tyr Asn Thr Leu  
 2660 2665 2670  
 Gly Ser Tyr Lys Cys Ala Cys Pro Ser Gly Phe Ser Phe Asp Gln Phe  
 2675 2680 2685  
 Ser Ser Ala Cys His Asp Val Asn Glu Cys Ser Ser Ser Lys Asn Pro  
 2690 2695 2700  
 Cys Asn Tyr Gly Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly Cys  
 2705 2710 2715 2720  
 Pro Pro Gly Tyr Tyr Arg Val Gly Gln Gly His Cys Val Ser Gly Met  
 2725 2730 2735  
 Gly Phe Asn Lys Gly Gln Tyr Leu Ser Leu Asp Thr Glu Val Asp Glu  
 2740 2745 2750  
 Glu Asn Ala Leu Ser Pro Glu Ala Cys Tyr Glu Cys Lys Ile Asn Gly  
 2755 2760 2765  
 Tyr Pro Lys Lys Asp Ser Arg Gln Lys Arg Ser Ile His Glu Pro Asp  
 2770 2775 2780  
 Pro Thr Ala Val Glu Gln Ile Ser Leu Glu Ser Val Asp Met Asp Ser  
 2785 2790 2795 2800  
 Pro Val Asn Met Lys Phe Asn Leu Ser His Leu Gly Ser Lys Glu His  
 2805 2810 2815  
 Ile Leu Glu Leu Arg Pro Ala Ile Gln Pro Leu Asn Asn His Ile Arg  
 2820 2825 2830  
 Tyr Val Ile Ser Gln Gly Asn Asp Asp Ser Val Phe Arg Ile His Gln  
 2835 2840 2845  
 Arg Asn Gly Leu Ser Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro  
 2850 2855 2860  
 Gly Thr Tyr Thr Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys  
 2865 2870 2875 2880  
 Glu Leu Lys Lys Leu Glu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly  
 2885 2890 2895

Glu Leu Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr  
 2900 2905 2910

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 <212> DNA  
 <213> Homo sapiens

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 tgtatcgagc tgatagctcg atgtgacgga gtctcggatt gcaaagacgg ggaggacgag 180  
 taccgctgtg tccgggtggg tggtcagaat gccgtgctcc aggtgttcac agctgcttcg 240  
 tggaagacca tgtgctccga tgactggaag ggtcactacg caaatgttgc ctgtgcccaa 300  
 ctgggtttcc caagctatgt gagttcagat aacctcagag tgagctcgct ggagggggcag 360  
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 caccactcag tatatgtgag ggagggatgt gcctctggcc acgtggttac cttgcagtgc 480  
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 ctctcgagcgt ggccctggca ggccagcctt cagttccagg gctaccacct gtgcgggggc 600  
 tctgtcatca cggccctgtg gatcatcact gctgcacact gtgtttatga cttgtacctc 660  
 cccaagtcac ggaccatcca ggtgggtcta gtttccctgt tggacaatcc agcccatcc 720  
 cacttggtgg agaagattgt ctaccacagc aagtacaagc caaagaggct gggcaatgac 780  
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 ctgcccact ctgaagagaa cttcccgat ggaaaagtgt gctggacgtc aggatggggg 900  
 gccacagagg atggagcagg tgacgcctcc cctgtcctga accacgcggc cgtccctttg 960  
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 gtgcccgcga ccacacccaa ctaatttttg tatttttagt agagacaggg tttcaccatg 1620  
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 agccaccaac agccactcag aaaagacgca ccagccaga agtgcagaac tgcagtcact 1920  
 gcacgttttc atctctaggg accagaacca aaccaccct ttctacttcc aagacttatt 1980  
 ttcacatgtg gggaggttaa tctaggaatg actcgtttaa ggcctatttt catgatttct 2040  
 ttgtagcatt tgggtgcttga cgtattattg tcctttgatt ccaaataata tgtttccttc 2100  
 cctcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2135



<210> 70  
 <211> 790  
 <212> PRT  
 <213> Sus scrofa

<400> 70

Asp Ser Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Phe Leu Phe Ser  
 1 5 10 15

Leu Ser Arg Lys Gln Val Ala Ala Arg Ser Val Glu Glu Cys Ala Ala  
 20 25 30

Lys Cys Glu Ala Glu Thr Asn Phe Ile Cys Arg Ala Phe Gln Tyr His  
 35 40 45

Ser Lys Asp Gln Gln Cys Val Val Met Ala Glu Asn Ser Lys Thr Ser  
 50 55 60

Pro Ile Ala Arg Met Arg Asp Val Val Leu Phe Glu Lys Arg Ile Tyr  
 65 70 75 80

Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr Thr  
 85 90 95

Ser Lys Thr Lys Ser Gly Val Ile Cys Gln Lys Trp Ser Val Ser Ser  
 100 105 110

Pro His Ile Pro Lys Tyr Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu  
 115 120 125

Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Lys Gly Pro Trp  
 130 135 140

Cys Tyr Thr Thr Asp Pro Glu Thr Arg Phe Asp Tyr Cys Asp Ile Pro  
 145 150 155 160

Glu Cys Glu Asp Glu Cys Met His Cys Ser Gly Glu His Tyr Glu Gly  
 165 170 175

Lys Ile Ser Lys Thr Met Ser Gly Ile Glu Cys Gln Ser Trp Gly Ser  
 180 185 190

Gln Ser Pro His Ala His Gly Tyr Leu Pro Ser Lys Phe Pro Asn Lys  
 195 200 205

Asn Leu Lys Met Asn Tyr Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro  
 210 215 220

Trp	Cys	Phe	Thr	Thr	Asp	Pro	Asn	Lys	Arg	Trp	Glu	Phe	Cys	Asp	Ile	225	230	235	240
Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Thr	Ser	Gly	Pro	Thr	Tyr	Gln	Cys	245	250	255	
Leu	Lys	Gly	Arg	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Val	Ser	Val	Thr	Ala	260	265	270	
Ser	Gly	His	Thr	Cys	Gln	Arg	Trp	Ser	Ala	Gln	Ser	Pro	His	Lys	His	275	280	285	
Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Glu	Glu	Asn	Tyr	290	295	300	
Cys	Arg	Asn	Pro	Asp	Gly	Glu	Thr	Ala	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	305	310	315	320
Ser	Glu	Val	Arg	Trp	Asp	Tyr	Cys	Lys	Ile	Pro	Ser	Cys	Gly	Ser	Ser	325	330	335	
Thr	Thr	Ser	Thr	Glu	His	Leu	Asp	Ala	Pro	Val	Pro	Pro	Glu	Gln	Thr	340	345	350	
Pro	Val	Ala	Gln	Asp	Cys	Tyr	Arg	Gly	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	355	360	365	
Thr	Ser	Ser	Thr	Thr	Ile	Thr	Gly	Arg	Lys	Cys	Gln	Ser	Trp	Val	Ser	370	375	380	
Met	Thr	Pro	His	Arg	His	Glu	Lys	Thr	Pro	Gly	Asn	Phe	Pro	Asn	Ala	385	390	395	400
Gly	Leu	Thr	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Asp	Lys	Ser	Pro	405	410	415	
Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Arg	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	420	425	430	
Lys	Lys	Cys	Ser	Glu	Thr	Glu	Gln	Gln	Val	Thr	Asn	Phe	Pro	Ala	Ile	435	440	445	
Ala	Gln	Val	Pro	Ser	Val	Glu	Asp	Leu	Ser	Glu	Asp	Cys	Met	Phe	Gly	450	455	460	
Asn	Gly	Lys	Arg	Tyr	Arg	Gly	Lys	Arg	Ala	Thr	Thr	Val	Ala	Gly	Val	465	470	475	480

Pro	Cys	Gln	Glu	Trp	Ala	Ala	Gln	Glu	Pro	His	Arg	His	Ser	Ile	Phe	485	490	495	
Thr	Pro	Glu	Thr	Asn	Pro	Arg	Ala	Gly	Leu	Glu	Lys	Asn	Tyr	Cys	Arg	500	505	510	
Asn	Pro	Asp	Gly	Asp	Asp	Asn	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Pro	515	520	525	
Gln	Lys	Leu	Phe	Asp	Tyr	Cys	Asp	Val	Pro	Gln	Cys	Val	Thr	Ser	Ser	530	535	540	
Phe	Asp	Cys	Gly	Lys	Pro	Lys	Val	Glu	Pro	Lys	Lys	Cys	Pro	Ala	Arg	545	550	555	560
Val	Val	Gly	Gly	Cys	Val	Ser	Ile	Pro	His	Ser	Trp	Pro	Trp	Gln	Ile	565	570	575	
Ser	Leu	Arg	Tyr	Arg	Tyr	Arg	Gly	His	Phe	Cys	Gly	Gly	Thr	Leu	Ile	580	585	590	
Ser	Pro	Glu	Trp	Val	Leu	Thr	Ala	Lys	His	Cys	Leu	Glu	Lys	Ser	Ser	595	600	605	
Ser	Pro	Ser	Ser	Tyr	Lys	Val	Ile	Leu	Gly	Ala	His	Glu	Glu	Tyr	His	610	615	620	
Leu	Gly	Glu	Gly	Val	Gln	Glu	Ile	Asp	Val	Ser	Lys	Leu	Phe	Lys	Glu	625	630	635	640
Pro	Ser	Glu	Ala	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Ser	Ser	Pro	Ala	Val	645	650	655	
Ile	Thr	Asp	Lys	Val	Ile	Pro	Ala	Cys	Leu	Pro	Thr	Pro	Asn	Tyr	Val	660	665	670	
Val	Ala	Asp	Arg	Thr	Ala	Cys	Tyr	Ile	Thr	Gly	Trp	Gly	Glu	Thr	Lys	675	680	685	
Gly	Thr	Tyr	Gly	Ala	Gly	Leu	Leu	Lys	Glu	Ala	Arg	Leu	Pro	Val	Ile	690	695	700	
Glu	Asn	Lys	Val	Cys	Asn	Arg	Tyr	Glu	Tyr	Leu	Gly	Gly	Lys	Val	Ser	705	710	715	720
Pro	Asn	Glu	Leu	Cys	Ala	Gly	His	Leu	Ala	Gly	Gly	Ile	Asp	Ser	Cys	725	730	735	

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr  
740 745 750

Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Leu Pro Asn  
755 760 765

Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu  
770 775 780

Glu Ile Met Arg Arg Asn  
785 790

<210> 71

<211> 812

<212> PRT

<213> Bos taurus

<400> 71

Met Leu Pro Ala Ser Pro Lys Met Glu His Lys Ala Val Val Phe Leu  
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Leu Leu Leu Phe Leu Lys Ser Gly Leu Gly Asp Leu Leu Asp Asp Tyr  
20 25 30

Val Asn Thr Gln Gly Ala Ser Leu Leu Ser Leu Ser Arg Lys Asn Leu  
35 40 45

Ala Gly Arg Ser Val Glu Asp Cys Ala Ala Lys Cys Glu Glu Glu Thr  
50 55 60

Asp Phe Val Cys Arg Ala Phe Gln Tyr His Ser Lys Glu Gln Gln Cys  
65 70 75 80

Val Val Met Ala Glu Asn Ser Lys Asn Thr Pro Val Phe Arg Met Arg  
85 90 95

Asp Val Ile Leu Tyr Glu Lys Arg Ile Tyr Leu Leu Glu Cys Lys Thr  
100 105 110

Gly Asn Gly Gln Thr Tyr Arg Gly Thr Thr Ala Glu Thr Lys Ser Gly  
115 120 125

Val Thr Cys Gln Lys Trp Ser Ala Thr Ser Pro His Val Pro Lys Phe  
130 135 140

Ser Pro Glu Lys Phe Pro Leu Ala Gly Leu Glu Glu Asn Tyr Cys Arg

145		150		155		160
Asn Pro Asp Asn Asp Glu Asn Gly Pro Trp Cys Tyr Thr Thr Asp Pro						
	165		170		175	
Asp Lys Arg Tyr Asp Tyr Cys Asp Ile Pro Glu Cys Glu Asp Lys Cys						
	180		185		190	
Met His Cys Ser Gly Glu Asn Tyr Glu Gly Lys Ile Ala Lys Thr Met						
	195		200		205	
Ser Gly Arg Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His						
	210		215		220	
Gly Tyr Ile Pro Ser Lys Phe Pro Asn Lys Asn Leu Lys Met Asn Tyr						
225		230		235		240
Cys Arg Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp						
	245		250		255	
Pro Gln Lys Arg Trp Glu Phe Cys Asp Ile Pro Arg Cys Thr Thr Pro						
	260		265		270	
Pro Pro Ser Ser Gly Pro Lys Tyr Gln Cys Leu Lys Gly Thr Gly Lys						
	275		280		285	
Asn Tyr Gly Gly Thr Val Ala Val Thr Glu Ser Gly His Thr Cys Gln						
	290		295		300	
Arg Trp Ser Glu Gln Thr Pro His Lys His Asn Arg Thr Pro Glu Asn						
305		310		315		320
Phe Pro Cys Lys Asn Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asn Gly						
	325		330		335	
Glu Lys Ala Pro Trp Cys Tyr Thr Thr Asn Ser Glu Val Arg Trp Glu						
	340		345		350	
Tyr Cys Thr Ile Pro Ser Cys Glu Ser Ser Pro Leu Ser Thr Glu Arg						
	355		360		365	
Met Asp Val Pro Val Pro Pro Glu Gln Thr Pro Val Pro Gln Asp Cys						
	370		375		380	
Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Ser Ser Thr Thr Ile						
385		390		395		400
Thr Gly Arg Lys Cys Gln Ser Trp Ser Ser Met Thr Pro His Arg His						

				405						410						415			
Leu	Lys	Thr	Pro	Glu	Asn	Tyr	Pro	Asn	Ala	Gly	Leu	Thr	Met	Asn	Tyr				
			420					425					430						
Cys	Arg	Asn	Pro	Asp	Ala	Asp	Lys	Ser	Pro	Trp	Cys	Tyr	Thr	Thr	Asp				
		435					440					445							
Pro	Arg	Val	Arg	Trp	Glu	Phe	Cys	Asn	Leu	Lys	Lys	Cys	Ser	Glu	Thr				
	450					455					460								
Pro	Glu	Gln	Val	Pro	Ala	Ala	Pro	Gln	Ala	Pro	Gly	Val	Glu	Asn	Pro				
465					470					475					480				
Pro	Glu	Ala	Asp	Cys	Met	Ile	Gly	Thr	Gly	Lys	Ser	Tyr	Arg	Gly	Lys				
			485					490						495					
Lys	Ala	Thr	Thr	Val	Ala	Gly	Val	Pro	Cys	Gln	Glu	Trp	Ala	Ala	Gln				
		500						505					510						
Glu	Pro	His	Gln	His	Ser	Ile	Phe	Thr	Pro	Glu	Thr	Asn	Pro	Gln	Ser				
	515						520					525							
Gly	Leu	Glu	Arg	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Val	Asn	Gly				
530						535					540								
Pro	Trp	Cys	Tyr	Thr	Met	Asn	Pro	Arg	Lys	Pro	Phe	Asp	Tyr	Cys	Asp				
545					550					555					560				
Val	Pro	Gln	Cys	Glu	Ser	Ser	Phe	Asp	Cys	Gly	Lys	Pro	Lys	Val	Glu				
			565						570					575					
Pro	Lys	Lys	Cys	Ser	Gly	Arg	Ile	Val	Gly	Gly	Cys	Val	Ser	Lys	Pro				
		580						585					590						
His	Ser	Trp	Pro	Trp	Gln	Val	Ser	Leu	Arg	Arg	Ser	Ser	Arg	His	Phe				
	595					600						605							
Cys	Gly	Gly	Thr	Leu	Ile	Ser	Pro	Lys	Trp	Val	Leu	Thr	Ala	Ala	His				
610						615					620								
Cys	Leu	Asp	Asn	Ile	Leu	Ala	Leu	Ser	Phe	Tyr	Lys	Val	Ile	Leu	Gly				
625					630					635					640				
Ala	His	Asn	Glu	Lys	Val	Arg	Glu	Gln	Ser	Val	Gln	Glu	Ile	Pro	Val				
			645					650					655						
Ser	Arg	Leu	Phe	Arg	Glu	Pro	Ser	Gln	Ala	Asp	Ile	Ala	Leu	Leu	Lys				

660	665	670
Leu Ser Arg Pro Ala Ile Ile Thr Lys Glu Val Ile Pro Ala Cys Leu		
675	680	685
Pro Pro Pro Asn Tyr Met Val Ala Ala Arg Thr Glu Cys Tyr Ile Thr		
690	695	700
Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Glu Gly Leu Leu Lys Glu		
705	710	715 720
Ala His Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Asn Glu Tyr		
725	730	735
Leu Asp Gly Arg Val Lys Pro Thr Glu Leu Cys Ala Gly His Leu Ile		
740	745	750
Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys		
755	760	765
Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu		
770	775	780
Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Pro		
785	790	795 800
Tyr Val Pro Trp Ile Glu Glu Thr Met Arg Arg Asn		
805	810	

<210> 72

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus  
Sequence

<400> 72

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln		
1	5	10 15
Val Ser Leu Gln Tyr Arg Gly Gly Gly Arg His Phe Cys Gly Gly Ser		
20	25	30
Leu Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly		
35	40	45

Ser Asp Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser  
 50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro  
 65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
 85 90 95

Lys Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
 100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
 115 120 125

Trp Gly Arg Thr Ser Glu Ser Gly Gly Ser Leu Pro Asp Thr Leu Gln  
 130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
 145 150 155 160

Ser Gly Gly Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu Glu  
 165 170 175

Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 180 185 190

Asn Asp Asn Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser Asp  
 195 200 205

Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser Ser  
 210 215 220

Tyr Leu Asp Trp Ile  
 225

<210> 73

<211> 2646

<212> DNA

<213> Homo sapiens

<400> 73

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 gattcaagat gttcttggca gccctgtcat tcagctatat tgctaaagca ctaggtggaa 180  
 tcattatgaa aatttccatc actcaaataag aaaggagatt tgacatatcc tcttctcttg 240



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ctggaagtat tttgacatct ttaccacatt tcttcatggg atattatagg tattctaaag 420
aaacccatat taatccatca gaaaattcaa catcaagttt atcaacctgt ttaattaatc 480
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gtattactta ggccaaaatc tggcctggat ttatgctata atatatattt tcatgttaag 2580
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2646

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<210> 74
<211> 691
<212> PRT
<213> Homo sapiens

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<400> 74

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Glu	Asn	Lys	Lys	Thr	Arg	Tyr	Cys	Asn	Gly	Leu	Lys	Met	Phe	Leu	Ala	
			20					25					30			
Ala	Leu	Ser	Leu	Ser	Phe	Ile	Ala	Lys	Thr	Leu	Gly	Ala	Ile	Ile	Met	
		35					40					45				
Lys	Ser	Ser	Ile	Ile	His	Ile	Glu	Arg	Arg	Phe	Glu	Ile	Ser	Ser	Ser	
	50					55					60					
Leu	Val	Gly	Phe	Ile	Asp	Gly	Ser	Phe	Glu	Ile	Gly	Asn	Leu	Leu	Val	
65					70				75						80	
Ile	Val	Phe	Val	Ser	Tyr	Phe	Gly	Ser	Lys	Leu	His	Arg	Pro	Lys	Leu	
				85					90					95		
Ile	Gly	Ile	Gly	Cys	Phe	Ile	Met	Gly	Ile	Gly	Gly	Val	Leu	Thr	Ala	
			100					105					110			
Leu	Pro	His	Phe	Phe	Met	Gly	Tyr	Tyr	Arg	Tyr	Ser	Lys	Glu	Thr	Asn	
		115					120					125				
Ile	Asn	Ser	Ser	Glu	Asn	Ser	Thr	Ser	Thr	Leu	Ser	Thr	Cys	Leu	Ile	
	130					135					140					
Asn	Gln	Ile	Leu	Ser	Leu	Asn	Arg	Ala	Ser	Pro	Glu	Ile	Val	Gly	Lys	
145					150					155					160	
Gly	Cys	Leu	Lys	Glu	Ser	Gly	Ser	Tyr	Met	Trp	Ile	Tyr	Val	Phe	Met	
				165					170					175		
Gly	Asn	Met	Leu	Arg	Gly	Ile	Gly	Glu	Thr	Pro	Ile	Val	Pro	Leu	Gly	
			180					185					190			
Leu	Ser	Tyr	Ile	Asp	Asp	Phe	Ala	Lys	Glu	Gly	His	Ser	Ser	Leu	Tyr	
		195					200					205				
Leu	Gly	Ile	Leu	Asn	Ala	Ile	Ala	Met	Ile	Gly	Pro	Ile	Ile	Gly	Phe	
	210					215					220					
Thr	Leu	Gly	Ser	Leu	Phe	Ser	Lys	Met	Tyr	Val	Asp	Ile	Gly	Tyr	Val	
225					230					235					240	
Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser	Arg	Trp	Val	Gly	
				245					250					255		

Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser  
 260 265 270  
 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys  
 275 280 285  
 Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu  
 290 295 300  
 Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys  
 305 310 315 320  
 Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro  
 325 330 335  
 Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr  
 340 345 350  
 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly  
 355 360 365  
 Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro  
 370 375 380  
 Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe  
 385 390 395 400  
 Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val  
 405 410 415  
 Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn  
 420 425 430  
 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val  
 435 440 445  
 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn  
 450 455 460  
 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr  
 465 470 475 480  
 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys  
 485 490 495  
 Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu  
 500 505 510

Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp  
 515 520 525

Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn  
 530 535 540

Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val  
 545 550 555 560

Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser  
 565 570 575

Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly  
 580 585 590

Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly  
 595 600 605

Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val  
 610 615 620

Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr  
 625 630 635 640

Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile  
 645 650 655

Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser  
 660 665 670

Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu  
 675 680 685

Thr His Cys  
 690

<210> 75

<211> 204

<212> DNA

<213> Rattus norvegicus

<400> 75

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 tggggggact tgcttcccgg gccaggacgg ctgtgactgc ccagagggct ggactggaat 180  
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<210> 76

<211> 91

<212> DNA

<213> Rattus norvegicus

<400> 76

tggtggacct ggatggcgg ctgccctttg tgcggcccct gcccacatt gcggtgctga 60  
gggatgagct gcccgcactc ttccaggatg a 91

<210> 77

<211> 1574

<212> PRT

<213> Rattus norvegicus

<400> 77

Met Pro Val Arg Ala Glu Ala Arg Ala Ala Trp Arg Val Val Ala Leu  
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Ala Leu Leu Leu Leu Pro Ala Met Pro Ala Ala Ser Pro Pro Leu Thr  
20 25 30

Pro Arg Pro Leu Gln Pro Ser Met Pro His Val Cys Ala Glu Gln Lys  
35 40 45

Leu Thr Leu Val Gly His Arg Gln Pro Cys Val Gln Ala Phe Ser Arg  
50 55 60

Ile Val Pro Val Trp Arg Arg Thr Gly Cys Ala Gln Gln Ala Trp Cys  
65 70 75 80

Ile Gly Gln Glu Arg Arg Thr Val Tyr Tyr Met Ser Tyr Arg Gln Val  
85 90 95

Tyr Ala Thr Glu Ala Arg Thr Val Phe Arg Cys Cys Pro Gly Trp Ser  
100 105 110

Gln Lys Pro Gly Gln Glu Gly Cys Leu Ser Asp Val Asp Glu Cys Ala  
115 120 125

Ser Ala Asn Gly Gly Cys Glu Gly Pro Cys Cys Asn Thr Val Gly Gly  
130 135 140

Phe Tyr Cys Arg Cys Pro Pro Gly Tyr Gln Leu Gln Gly Asp Gly Lys  
145 150 155 160

Thr	Cys	Gln	Asp	Val	Asp	Glu	Cys	Arg	Ala	His	Asn	Gly	Gly	Cys	Gln		165	170	175
His	Arg	Cys	Val	Asn	Thr	Pro	Gly	Ser	Tyr	Leu	Cys	Glu	Cys	Lys	Pro		180	185	190
Gly	Phe	Arg	Leu	His	Thr	Asp	Gly	Arg	Thr	Cys	Leu	Ala	Ile	Ser	Ser		195	200	205
Cys	Thr	Leu	Gly	Asn	Gly	Gly	Cys	Gln	His	Gln	Cys	Val	Gln	Leu	Thr		210	215	220
Val	Thr	Gln	His	Arg	Cys	Gln	Cys	Arg	Pro	Gln	Tyr	Gln	Leu	Gln	Glu		225	230	235
Asp	Gly	Arg	Arg	Cys	Val	Arg	Arg	Ser	Pro	Cys	Ala	Glu	Gly	Asn	Gly		245	250	255
Gly	Cys	Met	His	Ile	Cys	Gln	Glu	Leu	Arg	Gly	Leu	Ala	His	Cys	Gly		260	265	270
Cys	His	Pro	Gly	Tyr	Gln	Leu	Ala	Ala	Asp	Arg	Lys	Thr	Cys	Glu	Asp		275	280	285
Val	Asp	Glu	Cys	Ala	Leu	Gly	Leu	Ala	Gln	Cys	Ala	His	Gly	Cys	Leu		290	295	300
Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Val	Cys	His	Ala	Gly	Tyr	Glu	Leu		305	310	315
Gly	Ala	Asp	Gly	Arg	Gln	Cys	Tyr	Arg	Ile	Glu	Met	Glu	Ile	Val	Asn		325	330	335
Ser	Cys	Glu	Ala	Gly	Asn	Gly	Gly	Cys	Ser	His	Gly	Cys	Ser	His	Thr		340	345	350
Ser	Thr	Gly	Pro	Leu	Cys	Thr	Cys	Pro	Arg	Gly	Tyr	Glu	Leu	Asp	Glu		355	360	365
Asp	Gln	Lys	Thr	Cys	Ile	Asp	Ile	Asp	Asp	Cys	Ala	Asn	Ser	Pro	Cys		370	375	380
Cys	Gln	Gln	Ala	Cys	Ala	Asn	Thr	Pro	Gly	Gly	Tyr	Glu	Cys	Ser	Cys		385	390	395
Phe	Ala	Gly	Tyr	Arg	Leu	Asn	Thr	Asp	Gly	Cys	Gly	Cys	Glu	Asp	Val		405	410	415

Asp	Glu	Cys	Ala	Ser	Gly	His	Gly	Gly	Cys	Glu	His	His	Cys	Ser	Asn	420	425	430
Leu	Ala	Gly	Ser	Phe	Gln	Cys	Phe	Cys	Glu	Ala	Gly	Tyr	Arg	Leu	Asp	435	440	445
Glu	Asp	Arg	Arg	Gly	Cys	Thr	Ser	Leu	Glu	Glu	Ser	Val	Val	Asp	Leu	450	455	460
Asp	Gly	Arg	Leu	Pro	Phe	Val	Arg	Pro	Leu	Pro	His	Ile	Ala	Val	Leu	465	470	475 480
Arg	Asp	Glu	Leu	Pro	Arg	Leu	Phe	Gln	Asp	Asp	Tyr	Gly	Ala	Glu	Glu	485	490	495
Glu	Ala	Ala	Ala	Ala	Glu	Leu	Arg	Gly	Glu	His	Thr	Leu	Thr	Glu	Lys	500	505	510
Phe	Val	Cys	Leu	Asp	His	Ser	Phe	Gly	His	Asp	Cys	Ser	Leu	Thr	Cys	515	520	525
Asp	Asp	Cys	Arg	Asn	Gly	Gly	Thr	Cys	Phe	Pro	Gly	Gln	Asp	Gly	Cys	530	535	540
Asp	Cys	Pro	Glu	Gly	Trp	Thr	Gly	Ile	Ile	Cys	Asn	Glu	Thr	Cys	Pro	545	550	555 560
Pro	Asp	Thr	Phe	Gly	Lys	Asn	Cys	Ser	Ser	Pro	Cys	Thr	Cys	Gln	Asn	565	570	575
Gly	Gly	Thr	Cys	Asp	Pro	Val	Leu	Gly	Ala	Cys	Arg	Cys	Pro	Pro	Gly	580	585	590
Val	Ser	Gly	Ala	His	Cys	Glu	Asp	Gly	Cys	Pro	Lys	Gly	Phe	Tyr	Gly	595	600	605
Lys	His	Cys	Arg	Lys	Lys	Cys	His	Cys	Ala	Asn	Arg	Gly	Arg	Cys	His	610	615	620
Arg	Leu	Tyr	Gly	Ala	Cys	Leu	Cys	Asp	Pro	Gly	Leu	Tyr	Gly	Arg	Phe	625	630	635 640
Cys	His	Leu	Ala	Cys	Pro	Pro	Trp	Ala	Phe	Gly	Pro	Gly	Cys	Ser	Glu	645	650	655
Asp	Cys	Leu	Cys	Glu	Gln	Ser	His	Thr	Arg	Ser	Cys	Asn	Pro	Lys	Asp	660	665	670

Gly Ser Cys Ser Cys Lys Ala Gly Phe Gln Gly Glu Arg Cys Gln Ala	675	680	685
Glu Cys Glu Ser Gly Phe Phe Gly Pro Gly Cys Arg His Arg Cys Thr	690	695	700
Cys Gln Pro Gly Val Ala Cys Asp Pro Val Ser Gly Glu Cys Arg Thr	705	710	715
Gln Cys Pro Pro Gly Tyr Gln Gly Glu Asp Cys Gly Gln Glu Cys Pro	725	730	735
Val Gly Thr Phe Gly Val Asn Cys Ser Gly Ser Cys Ser Cys Val Gly	740	745	750
Ala Pro Cys His Arg Val Thr Gly Glu Cys Leu Cys Pro Pro Gly Lys	755	760	765
Thr Gly Glu Asp Cys Gly Ala Asp Cys Pro Glu Gly Arg Trp Gly Leu	770	775	780
Gly Cys Gln Glu Ile Cys Pro Ala Cys Glu His Gly Ala Ser Cys Asn	785	790	795
Pro Glu Thr Gly Thr Cys Leu Cys Leu Pro Gly Phe Val Gly Ser Arg	805	810	815
Cys Gln Asp Thr Cys Ser Ala Gly Trp Tyr Gly Thr Gly Cys Gln Ile	820	825	830
Arg Cys Ala Cys Ala Asn Asp Gly His Cys Asp Pro Thr Thr Gly Arg	835	840	845
Cys Ser Cys Ala Pro Gly Trp Thr Gly Leu Ser Cys Gln Arg Ala Cys	850	855	860
Asp Ser Gly His Trp Gly Pro Asp Cys Ile His Pro Cys Asn Cys Ser	865	870	875
Ala Gly His Gly Asn Cys Asp Ala Val Ser Gly Leu Cys Leu Cys Glu	885	890	895
Ala Gly Tyr Glu Gly Pro Arg Cys Glu Gln Ser Cys Arg Gln Gly Tyr	900	905	910
Tyr Gly Pro Ser Cys Glu Gln Lys Cys Arg Cys Glu His Gly Ala Ala	915	920	925



Cys Asp His Val Ser Gly Ala Cys Thr Cys Pro Ala Gly Trp Arg Gly  
 930 935 940

Ser Phe Cys Glu His Ala Cys Pro Ala Gly Phe Phe Gly Leu Asp Cys  
 945 950 955 960

Asp Ser Ala Cys Asn Cys Ser Ala Gly Ala Pro Cys Asp Ala Val Thr  
 965 970 975

Gly Ser Cys Ile Cys Pro Ala Gly Arg Trp Gly Pro Arg Cys Ala Gln  
 980 985 990

Ser Cys Pro Pro Leu Thr Phe Gly Leu Asn Cys Ser Gln Ile Cys Thr  
 995 1000 1005

Cys Phe Asn Gly Ala Ser Cys Asp Ser Val Thr Gly Gln Cys His Cys  
 1010 1015 1020

Ala Pro Gly Trp Met Gly Pro Thr Cys Leu Gln Ala Cys Pro Pro Gly  
 1025 1030 1035 1040

Leu Tyr Gly Lys Asn Cys Gln His Ser Cys Leu Cys Arg Asn Gly Gly  
 1045 1050 1055

Arg Cys Asp Pro Ile Leu Gly Gln Cys Thr Cys Pro Glu Gly Trp Thr  
 1060 1065 1070

Gly Leu Ala Cys Glu Asn Glu Cys Leu Pro Gly His Tyr Ala Ala Gly  
 1075 1080 1085

Cys Gln Leu Asn Cys Ser Cys Leu His Gly Gly Ile Cys Asp Arg Leu  
 1090 1095 1100

Thr Gly His Cys Leu Cys Pro Ala Gly Trp Thr Gly Asp Lys Cys Gln  
 1105 1110 1115 1120

Ser Ser Cys Val Ser Gly Thr Phe Gly Val His Cys Glu Glu His Cys  
 1125 1130 1135

Ala Cys Arg Lys Gly Ala Ser Cys His His Val Thr Gly Ala Cys Phe  
 1140 1145 1150

Cys Pro Pro Gly Trp Arg Gly Pro His Cys Glu Gln Ala Cys Pro Arg  
 1155 1160 1165

Gly Trp Phe Gly Glu Ala Cys Ala Gln Arg Cys Leu Cys Pro Thr Asn  
 1170 1175 1180

Ala Ser Cys His His Val Thr Gly Glu Cys Arg Cys Pro Pro Gly Phe  
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 Thr Gly Leu Ser Cys Glu Gln Ala Cys Gln Pro Gly Thr Phe Gly Lys  
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 Asp Cys Glu His Leu Cys Gln Cys Pro Gly Glu Thr Trp Ala Cys Asp  
 1220 1225 1230  
 Pro Ala Ser Gly Val Cys Thr Cys Ala Ala Gly Tyr His Gly Thr Gly  
 1235 1240 1245  
 Cys Leu Gln Arg Cys Pro Ser Gly Arg Tyr Gly Pro Gly Cys Glu His  
 1250 1255 1260  
 Ile Cys Lys Cys Leu Asn Gly Gly Thr Cys Asp Pro Ala Thr Gly Ala  
 1265 1270 1275 1280  
 Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp Cys Ser Leu Ala Cys  
 1285 1290 1295  
 Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His Val Cys Ala Cys Arg  
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 Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Ala Cys Ile Cys Ser Pro  
 1315 1320 1325  
 Gly Lys Thr Gly Val Arg Cys Glu His Gly Cys Pro Gln Asp Arg Phe  
 1330 1335 1340  
 Gly Lys Gly Cys Glu Leu Lys Cys Ala Cys Arg Asn Gly Gly Leu Cys  
 1345 1350 1355 1360  
 His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met Gly Pro  
 1365 1370 1375  
 His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala Cys Leu  
 1380 1385 1390  
 Leu Glu Cys Phe Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr Thr Gly  
 1395 1400 1405  
 Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu His Ser  
 1410 1415 1420  
 Cys Pro Ser Gly Phe His Gly Pro Gly Cys Gln Arg Val Cys Glu Cys  
 1425 1430 1435 1440

Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Gln Cys Leu Cys Pro  
1445 1450 1455

Ala Gly Phe His Gly Gln Phe Cys Glu Lys Gly Cys Glu Ser Gly Ser  
1460 1465 1470

Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys His Thr Gly Val Pro  
1475 1480 1485

Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg Thr Gly  
1490 1495 1500

Ala Ala Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro Gly Cys  
1505 1510 1515 1520

Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp Cys Asp Pro Ile Ser  
1525 1530 1535

Gly Gln Cys His Cys Val Asp Ser Tyr Met Gly Pro Thr Cys Arg Glu  
1540 1545 1550

Val Pro Thr Gln Ile Ser Ser Ser Arg Pro Ala Pro Gln His Pro Ser  
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Ser Arg Ala Met Lys His  
1570

<210> 78

<211> 1708

<212> DNA

<213> Homo sapiens

<400> 78

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gcgacaattg caattggagc agagcctgcg cgtttgcctg cggctgctgc atgcctggga 240  
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ccttccagca tgcacacca gtccacaaga cctcaaagag ttggagtttc tgaccaggc 360  
actggagaag gctgtacgag ttccaagagg catcactaag gccggagaga ga'gacaaggc 420  
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gcattcccca ggccaagctg gtggccatgc ttcagacacg agaccacca agggcctccg 540  
ccagaccacg gtgcctgcc aaggccaccc tgagcgccg ctgctgtcag tgggggatgg 600  
gaccctgtgt gggatgggag cccgaacccc caggcctggg gcgggcctca gggaccagca 660  
aatggcccca tccgctgctc ctcaggcccc agaagccttc aactcaagg agaaggggca 720  
cctgctgcgg ctgcctgcg cattcaggaa agcagcttcc cagaactcga gcctgtgggc 780  
ccagctcagt tccacacaga ccagtgattc cacggatgcc gccgctgcc aaaccagtt 840

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cctccagaac atgcagacag cttcaggcgg gccccagccc aggctcagtg ctgtggaggt 900
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<210> 79

<211> 1151

<212> PRT

<213> Gallus gallus

<400> 79

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Arg Ser Pro Thr Pro Pro Pro Arg Asn Pro Pro Thr Pro Pro Pro Ala
 1                      5                      10                      15

Pro Ser Pro Ala Pro Ala Pro Ala Pro Ala Pro Thr Ala Pro Pro Arg
          20                      25                      30

Pro Lys Trp Val Pro Ile Ala Glu Leu His Pro Ala Ala Pro Gln Pro
          35                      40                      45

Pro Pro Lys Trp Val Pro Ile Gly Gly Ala Pro Pro Pro Pro Gly Thr
          50                      55                      60

Glu Pro Thr Pro Pro Ser Lys Pro Thr Asp Gly Ala Asp Ala Ala Pro
65                      70                      75                      80

Lys Ala Ser Ala Glu Leu Thr Ser Pro Pro Pro Ala Ser Pro Ser Pro
          85                      90                      95

Pro Asp Gly Pro Lys Ala Pro Ser Gly Ala Gly Glu Ala Glu Ala Gly
          100                      105                      110

Thr Pro Pro Pro Ser Gln Gly Pro Ala Gly Thr Pro Pro Pro Ser Gln
          115                      120                      125

Gly Ala Ala Gly Ala Pro Lys Gly Asp Gly Thr Ala Gln Pro Ser Gly

```

130						135						140				
Thr	Lys	Ser	Gly	Ala	Asp	Gly	Lys	Pro	Ala	Ala	Gln	Asp	Val	Pro	Lys	
145					150					155					160	
Ala	Thr	Thr	Ala	Ala	Thr	Glu	Ala	Arg	Pro	Ala	Ser	Ala	Ala	Ser	Pro	
			165						170					175		
Thr	Val	Pro	Lys	Ala	Thr	Ala	Glu	Ala	Thr	Ala	Val	Thr	Ala	Ala	Ser	
			180					185					190			
Gln	Ser	Ala	Pro	Lys	Ala	Ala	Thr	Asp	Ala	Ala	Ala	Val	Thr	Ala	Ala	
	195						200					205				
Ser	Gln	Ser	Ala	Pro	Lys	Ala	Thr	Val	Glu	Val	Lys	Pro	Ala	Ala	Ala	
	210					215					220					
Ala	Val	Ala	Lys	Glu	Ala	Lys	Ala	Val	Thr	Ala	Ala	Ala	Ala	Ala	Pro	
225					230					235					240	
Lys	Ala	Thr	Ala	Glu	Ala	Lys	Pro	Ala	Pro	Val	Thr	Ser	Pro	Thr	Ile	
			245						250					255		
Pro	Cys	Ser	Ser	Ala	Glu	Ala	Lys	Pro	Leu	Thr	Ala	Ala	Ser	Pro	Thr	
		260						265						270		
Ala	Ser	Lys	Ala	Thr	Ala	Glu	Ala	Lys	Pro	Val	Pro	Ala	Thr	Ala	Ser	
	275						280					285				
Leu	Met	Ala	Thr	Lys	Val	Thr	Ala	Glu	Ala	Lys	Pro	Ala	Pro	Ser	Pro	
	290					295					300					
Ser	Val	Pro	Lys	Ala	Thr	Thr	Asp	Thr	Lys	Ala	Val	Thr	Ala	Thr	Ala	
305					310					315					320	
Pro	Lys	Ala	Gly	Pro	Asp	Val	Lys	Pro	Ala	Val	Ala	Val	Cys	Ala	Glu	
			325						330				335			
Ala	Lys	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Gln	Gln	Leu	Pro	Lys	Ala	Ala	
		340						345					350			
Ala	Ala	Ala	Ala	Pro	Thr	Gly	Thr	Glu	Leu	Lys	Pro	Ala	Thr	Ala	Pro	
	355						360					365				
Pro	His	Gly	Ser	Pro	Arg	Ala	Asn	Ser	His	Thr	Val	Thr	Val	Thr	Pro	
	370					375					380					
Pro	Asn	Val	Pro	Arg	Ala	Ala	Ala	Ala	Thr	Val	Pro	Thr	Ala	Gly	Ala	

385		390		395		400
Val Pro Lys Ala Ser Thr Gly Thr Thr	405	Pro Ala Ala Ala	410	Pro Gln Gln	415	
Pro Val Pro Lys Ala Ala Pro Val Thr	420	Pro Pro Ser Pro	425	Gln Gln Ala	430	
Val Pro Arg Ala Ala Thr Ala Ala Ala	435	Pro Val Thr Pro	440	Gln Gln	445	
Pro Val Thr Lys Ala Ala Thr Thr Thr	450	Asn Ala Thr Pro	455	Pro Pro Pro	460	Gln
Pro Ile Pro Lys Ala Ala Thr Thr Thr	465	Ala Thr Pro Val Thr	470	Pro	475	480
Gln Gln Pro Ile Pro Lys Ala Gly Thr	485	Asp Ala Ala Pro	490	Pro Pro Ala	495	
Val Pro Lys Ala Pro Ser Asp Gly Arg	500	Ala Ala Thr Pro	505	Gly Val Pro	510	
Asn Ala Ala Thr Asp Pro Gln Lys Pro	515	Pro Pro Thr Pro	520	Gln Ser Val	525	
Pro Ser Ala Val Thr Glu Pro Lys Pro	530	Gln Pro Arg Ala	535	Ala Pro Pro	540	
Pro Ser Asn Glu Ala Thr Pro Ala Val	545	Pro Ser Pro Ser	550	Pro Asn Leu	555	560
Lys Ser Pro Leu Pro Thr Ile Pro Lys	565	Pro Val Pro Leu	570	Met Ala Leu	575	
Thr Pro Gln Pro Val Thr Ala Gln Met	580	Val Thr Gln Leu	585	Ala Ala Thr	590	
Lys Pro Ser Pro Ile Val Pro Lys Ala	595	Ser Pro Lys Ala	600	Leu Met Thr	605	
Pro Pro Pro Pro Pro Pro Gly Leu	610	Pro Arg Ala Leu	615	Ala Ala Lys	620	
Leu Leu Gly Leu Pro Ser Ser Pro Val	625	Ala Ser Ala Met	630	His Ala Lys	635	640
Val Thr Pro Arg Pro Leu Pro Ala Ser		Pro Val Pro Met		Ala Ala Ser		



900	905	910
Thr Val Ala Gly Ser Pro Thr	Pro Pro Pro Pro Ile	Pro Pro Ser Pro
915	920	925
Thr Ala Gln Thr Ser Pro Gln	Pro Met Ser Lys Ser	Pro Pro Pro Asp
930	935	940
Pro Pro Lys Ala Pro Ser Ala	Ala Ala Gln Thr Ser	Pro Ala Ala His
945	950	955
Val Ala Asn Ala Ser Pro Gly	Val Thr Ala Val Ser	Pro Ala Pro Ile
965	970	975
Gly Val Thr Glu Ala Ser Pro	Ser Ala Asp Gly Ala Arg	Leu Ser Pro
980	985	990
Gly Pro Thr Ala Ala Thr Asp	Gly Pro Lys Ala Ser	Pro Ala Ala Thr
995	1000	1005
Ala Asp Val Thr Glu Ala Ala	Thr Asp Val Thr Ala	Ala Ala Thr Ala
1010	1015	1020
Val Pro Ala Glu Ala Ala Pro	Thr Lys Ala Lys Arg	Ser Ser Ser Ser
1025	1030	1035
Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser
1045	1050	1055
Ser Ser Ser Ser Asp Ser	Asp Ser Ser Ser Ser Ser	Ser Ser Glu Ser Asn
1060	1065	1070
Pro Ala Ser Pro Ala Pro	Ala Val Gly Asp Gly	Gln Gln Gln Met Thr
1075	1080	1085
Pro Gly Ala Ala Gln Ser	Val Pro Pro Val Thr	Glu Ala Ala Val Gln
1090	1095	1100
Glu Ala Ala Ala Ala Ala	Ala Ala Ala Gly Ala	Glu Arg Glu Gly
1105	1110	1115
Arg Pro Thr Arg Arg Lys	Lys Arg Thr Arg Ser	Ser Ser Ser Ser
1125	1130	1135
Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser Ser Ser	Ser Ser Ser Ser
1140	1145	1150



<210> 80  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 80

Met	Asn	Cys	Val	Cys	Arg	Leu	Val	Leu	Val	Val	Leu	Ser	Leu	Trp	Pro
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Asp	Thr	Ala	Val	Ala	Pro	Gly	Pro	Pro	Pro	Gly	Pro	Pro	Arg	Val	Ser
			20					25					30		
Pro	Asp	Pro	Arg	Ala	Glu	Leu	Asp	Ser	Thr	Val	Leu	Leu	Thr	Arg	Ser
		35					40					45			
Leu	Leu	Ala	Asp	Thr	Arg	Gln	Leu	Ala	Ala	Gln	Leu	Arg	Asp	Lys	Phe
	50					55					60				
Pro	Ala	Asp	Gly	Asp	His	Asn	Leu	Asp	Ser	Leu	Pro	Thr	Leu	Ala	Met
65					70					75					80
Ser	Ala	Gly	Ala	Leu	Gly	Ala	Leu	Gln	Leu	Pro	Gly	Val	Leu	Thr	Arg
				85				90						95	
Leu	Arg	Ala	Asp	Leu	Leu	Ser	Tyr	Leu	Arg	His	Val	Gln	Trp	Leu	Arg
			100					105					110		
Arg	Ala	Gly	Gly	Ser	Ser	Leu	Lys	Thr	Leu	Glu	Pro	Glu	Leu	Gly	Thr
		115					120					125			
Leu	Gln	Ala	Arg	Leu	Asp	Arg	Leu	Leu	Arg	Arg	Leu	Gln	Leu	Leu	Met
	130					135					140				
Ser	Arg	Leu	Ala	Leu	Pro	Gln	Pro	Pro	Pro	Asp	Pro	Pro	Ala	Pro	Pro
145					150					155				160	
Leu	Ala	Pro	Pro	Ser	Ser	Ala	Trp	Gly	Gly	Ile	Arg	Ala	Ala	His	Ala
				165					170					175	
Ile	Leu	Gly	Gly	Leu	His	Leu	Thr	Leu	Asp	Trp	Ala	Val	Arg	Gly	Leu
		180						185					190		
Leu	Leu	Leu	Lys	Thr	Arg	Leu									
		195													

<210> 81  
 <211> 1029

<212> DNA

<213> Homo sapiens

<400> 81

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ccctccctgt cagggcgtaa ttgagtcaaa ggcaggatca ggttccccgc cttccagtcc 180
aaaaatcccg ccaagagagc cccagagcag aggaaaatcc aaagtggaga gaggggaaga 240
aagagaccag tgagtcattc gtccagaagg cggggagagc agcagcggcc caagcaggag 300
ctgcagcgag ccgggtacct ggactcagcg gtagcaacct cgccccctgc aacaaaggca 360
gactgagcgc cagagaggac gtttccaact caaaaatgca ggctcaacag taccagcagc 420
agcgtcgaaa atttgcagct gccttcttgg cattcatttt catactggca gctgtggata 480
ctgctgaagc agggaagaaa gagaaaccag aaaaaaagt gaagaagtct gactgtggag 540
aatggcagtg gagtgtgtgt gtgccacca gtggagactg tgggctgggc acacgggagg 600
gcaactcgac tggagctgag tgcaagcaaa ccatgaagac ccagagatgt aagatcccct 660
gcaactggaa gaagcaattt ggcgcggagt gcaaatacca gttccaggcc tggggagaat 720
gtgacctgaa cacagccctg aagaccagaa ctggaagtct gaagcgagcc ctgcacaatg 780
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ctcaagcaga atctaagaag aagaaaaagg aaggcaagaa acaggagaag atgctggatt 900
aaaagatgtc acctgtggaa cataaaaagg acatcagcaa acaggatcag ttaactattg 960
catttatatg taccgtaggc ttgtattca aaaattatct atagctaagt acacaataag 1020
caaaaacaa 1029
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<210> 82

<211> 216

<212> PRT

<213> Homo sapiens

<400> 82

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Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1              5              10              15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20              25              30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35              40              45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50              55              60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
      65              70              75              80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
      85              90              95
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Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 83

<211> 346

<212> PRT

<213> Rattus norvegicus

<400> 83

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro  
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Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn  
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu  
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys  
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp  
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala  
85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr  
 100 105 110  
 Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala Met  
 115 120 125  
 Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser Ser  
 130 135 140  
 Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp Ala  
 145 150 155 160  
 Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr Tyr Gln Arg Leu Phe  
 165 170 175  
 His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu His Trp Pro Asn Gln  
 180 185 190  
 Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr Leu  
 195 200 205  
 Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His  
 210 215 220  
 Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys  
 225 230 235 240  
 Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Val Phe Gly Ile  
 245 250 255  
 Ser Trp Leu Pro His His Val Ile His Leu Trp Ala Glu Phe Gly Ala  
 260 265 270  
 Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His Cys  
 275 280 285  
 Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe Leu  
 290 295 300  
 Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys Arg Val  
 305 310 315 320  
 Cys Asn Glu Ser Pro His Gly Asp Ala Lys Glu Lys Asn Arg Ile Asp  
 325 330 335  
 Thr Pro Pro Ser Thr Asn Cys Thr His Val  
 340 345

<210> 84  
 <211> 1308  
 <212> DNA  
 <213> Bos taurus

<400> 84

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ccgaggccgc aggaggagcc ccagcggcgg ccgccacagc agcctgaagc tcgggagcct 180
cccggcaggg gccgcgcgtt ggtgccccac gagtacatgc tgtcaatcta caggacttac 240
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cagaagtatt tgtttgatgt gtccacgctc tcagacaaag aagagctggt gggcgcggac 420
gtgcggctgt ttccgccaggc gcccgctgcc ctggcgccgc cggcggccgc tccgcttgca 480
gctcttcgcc tgccagtcgc ccctgctgct ggaagcgcgg agcctggacc cgcaggggcg 540
ccccggcccc gctgggaagt ctccgacgtg tggcggggcc tgcgccccca gccctggaag 600
cagctgtgct tggagcttcg ggccgcgtgg ggccggcagc cggcgccgcg ggaggacgag 660
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tgcgtgccca ccaaattgac tcccatcagc atcttgtaca tcgacgcggg caataatgtg 1260
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<210> 85  
 <211> 436  
 <212> PRT  
 <213> Bos taurus

<400> 85

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Arg Ala Ser Ala Glu Leu Gly Ser Ala Lys Gly Met Arg Thr Arg Lys
  1              5              10              15

Glu Gly Arg Met Pro Arg Ala Pro Arg Glu Asn Ala Thr Ala Arg Glu
          20              25              30

Pro Leu Asp Arg Gln Glu Pro Pro Pro Arg Pro Gln Glu Glu Pro Gln
          35              40              45

Arg Arg Pro Pro Gln Gln Pro Glu Ala Arg Glu Pro Pro Gly Arg Gly
  
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50		55		60
Pro Arg Leu Val Pro His Glu Tyr Met Leu Ser Ile Tyr Arg Thr Tyr				
65		70		75 80
Ser Ile Ala Glu Lys Leu Gly Ile Asn Ala Ser Phe Phe Gln Ser Ser				
	85		90	95
Lys Ser Ala Asn Thr Ile Thr Ser Phe Val Asp Arg Gly Leu Asp Asp				
	100		105	110
Leu Ser His Thr Pro Leu Arg Arg Gln Lys Tyr Leu Phe Asp Val Ser				
	115		120	125
Thr Leu Ser Asp Lys Glu Glu Leu Val Gly Ala Asp Val Arg Leu Phe				
	130		135	140
Arg Gln Ala Pro Ala Ala Leu Ala Pro Pro Ala Ala Ala Pro Leu Ala				
	145		150	155 160
Ala Leu Arg Leu Pro Val Ala Pro Ala Ala Gly Ser Ala Glu Pro Gly				
	165		170	175
Pro Ala Gly Ala Pro Arg Pro Gly Trp Glu Val Phe Asp Val Trp Arg				
	180		185	190
Gly Leu Arg Pro Gln Pro Trp Lys Gln Leu Cys Leu Glu Leu Arg Ala				
	195		200	205
Ala Trp Gly Gly Glu Pro Gly Ala Ala Glu Asp Glu Ala Arg Thr Pro				
	210		215	220
Gly Pro Gln Gln Pro Pro Pro Pro Asp Leu Arg Ser Leu Gly Phe Gly				
	225		230	235 240
Arg Arg Val Arg Thr Pro Gln Glu Arg Ala Leu Leu Val Val Phe Ser				
	245		250	255
Arg Ser Gln Arg Lys Thr Leu Phe Ala Glu Met Arg Glu Gln Leu Gly				
	260		265	270
Ser Ala Thr Glu Val Val Gly Pro Gly Gly Gly Ala Glu Gly Ser Gly				
	275		280	285
Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Gly Thr Pro Asp Ala				
	290		295	300
Gly Leu Trp Ser Pro Ser Pro Gly Arg Arg Arg Arg Thr Ala Phe Ala				

305		310		315		320
Ser Arg His Gly Lys Arg His Gly Lys Lys Ser Arg Leu Arg Cys Ser						
	325		330		335	
Lys Lys Pro Leu His Val Asn Phe Lys Glu Leu Gly Trp Asp Asp Trp						
	340		345		350	
Ile Ile Ala Pro Leu Glu Tyr Glu Ala Tyr His Cys Glu Gly Val Cys						
	355		360		365	
Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile Ile						
	370		375		380	
Gln Thr Leu Met Asn Ser Met Asp Pro Gly Ser Thr Pro Pro Ser Cys						
	385		390		395	400
Cys Val Pro Thr Lys Leu Thr Pro Ile Ser Ile Leu Tyr Ile Asp Ala						
	405		410		415	
Gly Asn Asn Val Val Tyr Asn Glu Tyr Glu Glu Met Val Val Glu Ser						
	420		425		430	
Cys Gly Cys Arg						
	435					